

SEQUENCE LISTING

<110> Regents of the University of California, The
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Valerie, Kickhoefer A.
Sujna, Raval-Fernandes
Phoebe, Stewart L.

<120> Vault and Vault-like Carrier Molecules

<130> 14399-1PCT

<140> to be assigned

<141> 2004-03-10

<150> 60/453,800

<151> 2003-03-10

<160> 143

<170> PatentIn version 3.2

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<212> PRT

<213> Homo sapiens

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Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
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Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
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Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
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Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp

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Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr 180 185 190		
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Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly 225 230 235 240		
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Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly 290 295 300		
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Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
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Gln Lys Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser
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Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met
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Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys
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Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu
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Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn
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Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His
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Val Glu Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu
 385 390 395 400

Gln Asn His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg
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Val Gly Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn
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Val Arg Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile
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Leu Cys Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val
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Gln Arg Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp
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Thr Arg Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp
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Leu His Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp
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Asp Asp Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr
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Ser Lys Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser
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Thr Lys Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu
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Asp Val His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile
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Ser Leu Leu Tyr Pro Ala Arg Gly Ser Arg Asn Ile Leu Leu Val Ser
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Asn Gln Cys Leu Ala Thr Leu Pro Asp Leu Lys Thr Met Glu Lys Pro
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His Gly Tyr Val Ser Ala His Pro Asp Ile Leu Ser Leu Glu Asn Gln
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Cys Leu Ala Thr Leu Ser Asp Leu Lys Thr Met Glu Lys Pro His Gly
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Ala Ala Pro His Arg Ile Ser Leu His Gly Ile Asp Leu Arg Trp Gly
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Cys Thr Tyr Leu Arg Gly Gln Leu Lys Glu Pro Gly Ala Leu Pro				
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Ser Thr Tyr Arg Ser Leu Val Trp Glu Leu Gln Gln Arg Leu Leu				
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Pro Lys Ser Ala Glu Ser Leu His Pro Gly Gln Thr Gln Val Leu				
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Ile Ile Asp Gly Ala Asp Arg Leu Val Asp Gln Asn Gly Gln Leu				
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Ile Ser Asp Trp Ile Pro Lys Lys Leu Pro Arg Cys Val His Leu				
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Val Leu Ser Val Ser Ser Asp Ala Gly Leu Gly Glu Thr Leu Glu				
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Gln Ser Gln Gly Ala His Val Leu Ala Leu Gly Pro Leu Glu Ala				
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Ser Ala Arg Ala Arg Leu Val Arg Glu Glu Leu Ala Leu Tyr Gly				
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Lys Arg Leu Glu Glu Ser Pro Phe Asn Asn Gln Met Arg Leu Leu				
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Leu Val Lys Arg Glu Ser Gly Arg Pro Leu Tyr Leu Arg Leu Val				
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Thr Asp His Leu Arg Leu Phe Thr Leu Tyr Glu Gln Val Ser Glu				
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Arg Leu Arg Thr Leu Pro Ala Thr Val Pro Leu Leu Leu Gln His				
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Asp Gln Leu His Gly Val Leu Ser Val Trp Arg Thr Leu Pro Lys
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Gly Thr Lys Ser Trp Glu Glu Ala Val Ala Ala Gly Asn Ser Gly
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Asp Pro Tyr Pro Met Gly Pro Phe Ala Cys Leu Val Gln Ser Leu
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Arg Ser Leu Leu Gly Glu Gly Pro Leu Glu Arg Pro Gly Ala Arg
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Leu Cys Leu Pro Asp Gly Pro Leu Arg Thr Ala Ala Lys Arg Cys
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Tyr Gly Lys Arg Pro Gly Leu Glu Asp Thr Ala His Ile Leu Ile
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Ala Ala Gln Leu Trp Lys Thr Cys Asp Ala Asp Ala Ser Gly Thr
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Phe Arg Ser Cys Pro Pro Glu Ala Leu Gly Asp Leu Pro Tyr His
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Leu Leu Gln Ser Gly Asn Arg Gly Leu Leu Ser Lys Phe Leu Thr
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Asn Leu His Val Val Ala Ala His Leu Glu Leu Gly Leu Val Ser
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Arg Leu Leu Glu Ala His Ala Leu Tyr Ala Ser Ser Val Pro Lys
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Glu Glu Gln Lys Leu Pro Glu Ala Asp Val Ala Val Phe Arg Thr
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Phe Leu Arg Gln Gln Ala Ser Ile Leu Ser Gln Tyr Pro Arg Leu
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Ala Phe Pro Ala His His Gly Phe Val Ala Ala Ala Leu Phe Leu 1880 1885 1890		
His Ala Gly Cys Gln Leu Leu Thr Ala Gly Glu Asp Gly Lys Val 1895 1900 1905		
Gln Val Trp Ser Gly Ser Leu Gly Arg Pro Arg Gly His Leu Gly 1910 1915 1920		
Ser Leu Ser Leu Ser Pro Ala Leu Ser Val Ala Leu Ser Pro Asp 1925 1930 1935		
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Tyr Lys Ile Ser Ser Gly Ser Gln Gly Ala Gln Gly Gln Ala Leu 1955 1960 1965		
Asp Val Ala Val Ser Ala Leu Ala Trp Leu Ser Pro Lys Val Leu 1970 1975 1980		
Val Ser Gly Ala Glu Asp Gly Ser Leu Gln Gly Trp Ala Leu Lys 1985 1990 1995		
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Pro Val Leu Gly Leu Ala Thr Ser Gln Glu Leu Leu Ala Ser Ala 2015 2020 2025		
Ser Glu Asp Phe Thr Val Gln Leu Trp Pro Arg Gln Leu Leu Thr 2030 2035 2040		
Arg Pro His Lys Ala Glu Asp Phe Pro Cys Gly Thr Glu Leu Arg 2045 2050 2055		

Gly His Glu Gly Pro Val Ser Cys Cys Ser Phe Ser Thr Asp Gly
 2060 2065 2070

Gly Ser Leu Ala Thr Gly Gly Arg Asp Arg Ser Leu Leu Cys Trp
 2075 2080 2085

Asp Val Arg Thr Pro Lys Thr Pro Val Leu Ile His Ser Phe Pro
 2090 2095 2100

Ala Cys His Arg Asp Trp Val Thr Gly Cys Ala Trp Thr Lys Asp
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Glu Leu Thr Ser Ile Pro Ala His Ser Gly Pro Ile Ser His Cys
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Lys Glu Ala Asp Asp Thr Cys Ile Pro Arg Ser Ser Ala Ala Val
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Cys Leu Glu Pro Trp Leu Gly Ala Asn Ser Thr Leu Gln Leu Ala		
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Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
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Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
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Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
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Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
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Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
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Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
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Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
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Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
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Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
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Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
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Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
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Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
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Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
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Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
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Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
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Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
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Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
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Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
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Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
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Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
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Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
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Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
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Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr

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Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg 500	505	510
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr 515	520	525
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn 530	535	540
Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys 545	550	555
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala 565	570	575
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His 580	585	590
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met 595	600	605
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp 610	615	620
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 625	630	635
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 645	650	655
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 660	665	670
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675	680	685
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 690	695	700
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly 705	710	715
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Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
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Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 755 760 765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
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Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 785 790 795 800

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
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Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
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<211> 2586

<212> DNA

<213> Rattus norvegicus

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<400> 12

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Leu Lys Asn Arg Cys Leu Thr Met Leu Ser Asp Ile Gln Pro Leu Glu
          20           25           30

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Lys Ile His Gly Gln Arg Ser Val Asn Pro Asp Ile Leu Ser Leu Glu
          35           40           45

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Asn Arg Cys Leu Thr Leu Leu Pro Asp Leu Gln Pro Met Glu Lys Ile
          50           55           60

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His Gly Gln Arg Ser Val His Pro Asp Ile Leu Ser Ser Glu Asn Arg
65           70           75           80

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Cys Leu Thr Leu Leu Pro Asp Leu Gln Ser Leu Glu Lys Leu Cys Gly
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His Met Ser Ser His Pro Asp Val Leu Ser Leu Glu Asn Arg Cys Leu
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Ala Thr Leu Pro Thr Val Lys Arg Thr Val Ser Ser Gly Pro Leu Leu
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Gln Cys Leu His Arg Ser His Thr Ala Gln Ala Asp Leu Arg Asp Pro
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Cys Phe Leu Lys Glu Leu Asp Leu Pro Thr Gly Pro Arg Ala Leu Lys
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Ser Met Ser Ala Thr Ala Arg Val Gln Glu Val Ala Leu Gly Gln Arg
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Cys Val Ser Glu Gly Lys Glu Leu Gln Glu Glu Lys Glu Ser Ala Glu
 195 200 205

Val Pro Met Pro Leu Tyr Ser Leu Ser Leu Gly Gly Glu Glu Glu Glu
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Val Val Gly Ala Pro Val Leu Lys Leu Thr Ser Gly Asp Ser Asp Ser
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His Pro Glu Thr Thr Asp Gln Ile Leu Gln Glu Lys Lys Met Ala Leu
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Leu Thr Leu Leu Cys Ser Ala Met Ala Ser Ser Val Asn Val Lys Asp
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Ala Ser Asp Pro Thr Arg Ala Ser Ile His Glu Val Cys Ser Ala Leu
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Ala Pro Leu Glu Pro Glu Phe Ile Leu Lys Ala Ser Leu Tyr Ala Arg
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Gln Gln Leu Asn Leu Arg Asp Ile Ala Asn Ile Val Leu Ala Val Ala
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Ile Val His Leu Pro Ser Asp Trp Ile Gln Val Ala Glu Phe Tyr Gln
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Ser Leu Ala Glu Gly Asp Glu Lys Lys Leu Val Pro Leu Pro Ala Cys
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Leu Ala Lys Tyr Asn Pro Arg Lys His Arg Ser Lys Thr Arg Ser Arg
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Gln Pro Pro Arg Pro Gln Arg Thr Lys Pro Pro Phe Ser Glu Ser Gly
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Lys Cys Phe Pro Lys Ser Val Trp Pro Leu Lys Asn Glu Gln Ile Ser
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Phe Glu Ala Ala Tyr Asn Ala Val Ser Glu Lys Lys Arg Leu Pro Arg
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Phe Thr Leu Lys Lys Leu Val Glu Gln Leu His Ile His Glu Pro Ala
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Gln His Glu Lys Ser Val Ile His Ser Arg Gln Phe Pro Phe Arg Phe
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Ile Arg Asn Ser Lys Lys Ile Lys Arg Pro Ala Asn Pro Arg Tyr Leu

43/429

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Pro Pro Gly Lys Thr Lys Val Ser Pro Leu Arg Pro Leu Glu Glu Asn
885 890 895

Asn Pro Gly Pro Phe Val Pro Ile Ser Gln His Gly Trp Arg Asn Ile
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Arg Leu Phe Ile Ser Ser Thr Phe Arg Asp Met His Gly Glu Arg Asp
915 920 925

Leu Leu Met Arg Ser Val Leu Pro Ala Leu Gln Ala Arg Ala Phe Pro
930 935 940

His Arg Ile Ser Leu His Ala Ile Asp Leu Arg Trp Gly Ile Thr Glu
945 950 955 960

Glu Glu Thr Arg Arg Asn Arg Gln Leu Glu Val Cys Leu Gly Glu Val
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Glu Asn Ser Gln Leu Phe Val Gly Ile Leu Gly Ser Arg Tyr Gly Tyr
980 985 990

Thr Pro Pro Ser Tyr Asp Leu Pro Asp His Pro His Phe His Trp Thr
995 1000 1005

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Leu Ile Tyr Phe Arg Asp Pro Gly Phe Leu Ser Ser Val Pro Asp
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Val Trp Lys Pro Asp Phe Ile Ser Glu Ser Glu Glu Ala Ala His
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Arg Val Ser Glu Leu Lys Arg Phe Leu Gln Glu Gln Lys Glu Val
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Thr Cys	Arg Arg Tyr Ser Cys	Glu Trp Gly Gly Val	Ala Ala Gly
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Arg Pro	Tyr Thr Gly Gly Leu	Glu Glu Phe Gly Gln	Leu Val Leu
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Gln Ala	Ser Phe Gln Gln Leu	Lys Ser Pro Pro Ser	Pro Ala Arg
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Pro Arg	Leu Leu Gln Asp Thr	Val Gln Gln Leu Met	Leu Pro His
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Gly Arg	Leu Ser Leu Val Ile	Gly Gln Ala Gly Gln	Gly Lys Thr
1175	1180	1185	
Ala Phe	Leu Ala Ser Leu Val	Ser Ala Leu Lys Val	Pro Asp Gln
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Pro Asn	Val Ala Pro Phe Val	Phe Phe His Phe Ser	Ala Ala Arg
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Pro Asp	Gln Cys Leu Ala Phe	Asn Leu Leu Arg Arg	Leu Cys Thr
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His Leu	His Gln Lys Leu Gly	Glu Pro Ser Ala Leu	Pro Ser Thr
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Tyr Arg	Gly Leu Val Trp Glu	Leu Gln Gln Lys Leu	Leu Leu Lys
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Ser Ala	Gln Trp Leu Gln Pro	Gly Gln Thr Leu Val	Leu Ile Ile
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Asp Gly	Ala Asp Lys Leu Val	Asp His Asn Gly Gln	Leu Ile Ser
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Asp Trp	Ile Pro Lys Ser Leu	Pro Arg Arg Val His	Leu Val Leu

1295	1300	1305
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Arg Ala 1340	Gln Leu Val Arg Glu 1345	Glu Leu Ala Leu Tyr Gly Lys Arg 1350
Leu Glu 1355	Glu Ser Pro Phe Asn 1360	Asn Gln Met Arg Leu Leu Leu Ala 1365
Lys Gln 1370	Gly Ser Ser Leu Pro 1375	Leu Tyr Leu His Leu Val Thr Asp 1380
Tyr Leu 1385	Arg Leu Phe Thr Leu 1390	Tyr Glu Gln Val Ser Glu Arg Leu 1395
Arg Thr 1400	Leu Pro Ala Thr Leu 1405	Pro Leu Leu Leu Gln His Ile Leu 1410
Ser Thr 1415	Leu Glu Gln Glu His 1420	Gly His Asn Val Leu Pro Gln Ala 1425
Leu Thr 1430	Ala Leu Glu Val Thr 1435	His Ser Gly Leu Thr Val Asp Gln 1440
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Lys Ser 1460	Trp Glu Glu Ala Val 1465	Ala Ala Ser His Ser Gly Asn Leu 1470
Tyr Pro 1475	Leu Ala Pro Phe Ala 1480	Tyr Leu Val Gln Ser Leu Arg Ser 1485
Leu Leu 1490	Gly Glu Gly Pro Val 1495	Glu Arg Pro Gly Ala Arg Leu Cys 1500
Leu Ser 1505	Asp Gly Pro Leu Arg 1510	Thr Ala Val Lys Arg Arg Tyr Gly 1515

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 1895 1900 1905
 Arg Phe Leu Thr Ala Gly Glu Asp Gly Lys Ala Gln Leu Trp Ser
 1910 1915 1920
 Gly Phe Leu Gly Arg Pro Arg Gly Cys Leu Gly Ser Leu Tyr Leu
 1925 1930 1935
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 1940 1945 1950
 Ala Val Gly Tyr Arg Gly Asp Gly Ile Lys Ile Tyr Arg Ile Ser

1955	1960	1965
Ser Gly 1970	Pro Gln Glu Ala Gln 1975	Cys Gln Glu Leu Asn Val Ala Val 1980
Ser Ala 1985	Leu Val Trp Leu Ser 1990	Pro Ser Val Leu Val Ser Gly Ala 1995
Glu Asp 2000	Gly Ser Leu His Gly 2005	Trp Met Leu Arg Arg Asn Ser Leu 2010
Gln Ser 2015	Leu Trp Leu Ser Ser 2020	Val Cys Gln Lys Pro Val Leu Gly 2025
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Val Glu 2060	Glu Leu Pro Cys Ala 2065	Ala Glu Leu Arg Gly His Glu Gly 2070
Pro Val 2075	Cys Cys Cys Ser Phe 2080	Ser Pro Asp Gly Arg Ile Leu Ala 2085
Thr Ala 2090	Gly Arg Asp Arg Asn 2095	Leu Leu Cys Trp Asp Val Lys Val 2100
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Asp Trp 2120	Ile Thr Gly Cys Thr 2125	Trp Thr Lys Asp Asn Ile Leu Ile 2130
Ser Cys 2135	Ser Ser Asp Gly Ser 2140	Val Gly Leu Trp Asn Pro Glu Ala 2145
Gly Gln 2150	Gln Leu Gly Gln Phe 2155	Pro Gly His Gln Ser Ala Val Ser 2160
Ala Val 2165	Val Ala Val Glu Glu 2170	His Ile Val Ser Val Ser Arg Asp 2175

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<210> 14

<211> 143

<212> RNA

<213> Rattus norvegicus

<400> 14

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<210> 15
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 15

Met Ala Gly Cys Gly Cys Pro Cys Gly Cys Gly Ala
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<210> 16
 <211> 905
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 16

Met Ala Gly Cys Gly Cys Pro Cys Gly Cys Gly Ala Met Ala Thr Glu
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Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys Thr Tyr Ile
 35 40 45

Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met Arg Met Val Thr
 50 55 60

Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro Val Ser Arg Asp
 65 70 75 80

Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln Val Arg Leu Arg
 85 90 95

His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro Phe Pro Leu Tyr
 100 105 110

Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln Val Val Leu
 115 120 125

Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe Glu Asp Lys
 130 135 140

Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu Phe Glu Gly Pro
 145 150 155 160

Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val Glu Ile Ile Gln
 165 170 175

Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu Arg Ala Arg Lys
 180 185 190

Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr Gly Glu Glu Trp
 195 200 205

Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val Phe Glu Glu Val
 210 215 220

Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr Ala Leu His
 225 230 235 240

Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly Val Ser Arg Arg
 245 250 255

Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu Ala His Val
 260 265 270

Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile Thr Thr Leu
 275 280 285

Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly Pro Asp Gly
 290 295 300

Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu Lys Ser Phe
 305 310 315 320

Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln Asp Val Tyr
 325 330 335

Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala Leu Gln Pro Leu
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Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln Ala Gly Asp His
 355 360 365

Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala Lys Val Glu

59/429

Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr Ser Glu Ala Lys
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Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp Gln Ala Val Phe
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Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln Ser Val Glu
 645 650 655

Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser Val Gln Leu
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Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala Lys His Glu
 675 680 685

Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu Arg Gln Lys
 690 695 700

Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu Leu Leu Glu
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Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly Thr Ala Lys Ala
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Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly Glu Gly Ser
 740 745 750

Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile Glu Thr Glu
 755 760 765

Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu Glu Leu Val Tyr
 770 775 780

Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln Leu Ala
 785 790 795 800

Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu Ala Ile Gly Pro
 805 810 815

Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met Gln Val Lys
 820 825 830

Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr Asp Gly Ser
 835 840 845

Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu Leu Gly Met Gly
 850 855 860

Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser Gly Pro Ser Pro
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Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro Gln Ala Pro Gly
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Asp Asn His Val Val Pro Val Leu Arg
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<210> 17
 <211> 2718
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 17
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 cgcacgttga ccgtcccccc acgtcactac tgcacagtgg ccaaccctgt gtctcgggat 240
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2718

<210> 18
 <211> 873
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 18

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 20 25 30

Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys Thr Tyr Ile
 35 40 45

Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg Met Val Thr
 50 55 60

Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val Ser Arg Asp
 65 70 75 80

Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val Arg Leu Arg
 85 90 95

His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe Pro Leu Tyr
 100 105 110

Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln Val Val Leu
 115 120 125

Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe Glu Asp Lys
 130 135 140

Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe Glu Gly Pro
 145 150 155 160

Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu Ile Ile Gln
 165 170 175

Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg Ala Arg Lys

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Leu	Val	Arg	Ser	Val	Gly	Ala	Tyr	Leu	Pro	Ala	Val	Phe	Glu	Glu	Val
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Leu	Asp	Leu	Val	Asp	Ala	Val	Ile	Leu	Thr	Glu	Lys	Thr	Ala	Leu	His
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Leu	Arg	Ala	Leu	Gln	Asn	Phe	Arg	Asp	Leu	Arg	Gly	Val	Leu	His	Arg
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Thr	Gly	Glu	Glu	Trp	Leu	Val	Thr	Val	Gln	Asp	Thr	Glu	Ala	His	Val
			260						265					270	
Pro	Asp	Val	Tyr	Glu	Glu	Val	Leu	Gly	Val	Val	Pro	Ile	Thr	Thr	Leu
		275					280					285			
Gly	Pro	Arg	His	Tyr	Cys	Val	Ile	Leu	Asp	Pro	Met	Gly	Pro	Asp	Gly
	290					295					300				
Lys	Asn	Gln	Leu	Gly	Gln	Lys	Arg	Val	Val	Lys	Gly	Glu	Lys	Ser	Phe
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Phe	Leu	Gln	Pro	Gly	Glu	Arg	Leu	Glu	Arg	Gly	Ile	Gln	Asp	Val	Tyr
				325					330					335	
Val	Leu	Ser	Glu	Gln	Gln	Gly	Leu	Leu	Leu	Lys	Ala	Leu	Gln	Pro	Leu
			340					345					350		
Glu	Glu	Gly	Glu	Ser	Glu	Glu	Lys	Val	Ser	His	Gln	Ala	Gly	Asp	Cys
		355					360					365			
Trp	Leu	Ile	Arg	Gly	Pro	Leu	Glu	Tyr	Val	Pro	Ser	Ala	Lys	Val	Glu
	370					375					380				
Val	Val	Glu	Glu	Arg	Gln	Ala	Ile	Pro	Leu	Asp	Gln	Asn	Glu	Gly	Ile
385					390					395					400
Tyr	Val	Gln	Asp	Val	Lys	Thr	Gly	Lys	Val	Arg	Ala	Val	Ile	Gly	Ser
				405					410					415	

Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys Glu Leu Pro
 420 425 430

Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro Leu Ala Asp
 435 440 445

Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser Ala Pro Arg
 450 455 460

Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn Ala Ala Val
 465 470 475 480

Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val Phe Gly Pro
 485 490 495

Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val Leu Ser Leu
 500 505 510

Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala Leu Cys Leu
 515 520 525

Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile Glu Thr Ala
 530 535 540

Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp His Phe Glu
 545 550 555 560

Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys Leu Phe Ser Val
 565 570 575

Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser Arg Val Arg
 580 585 590

Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys Asn Ser Ala
 595 600 605

Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met Ser Glu Asp Thr
 610 615 620

Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp Gln Ala Val Phe
 625 630 635 640

Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln Ser Val Glu
 645 650 655

Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser Val Gln Leu
 660 665 670

Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala Lys His Glu
 675 680 685

Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu Arg Gln Lys
 690 695 700

Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu Leu Leu Glu
 705 710 715 720

Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly Asn Ala Lys Ala
 725 730 735

Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly Glu Gly Ser
 740 745 750

Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile Glu Thr Glu
 755 760 765

Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met Glu Leu Ile Tyr
 770 775 780

Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln Leu Ala
 785 790 795 800

Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu Ala Leu Gly Pro
 805 810 815

Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met Gln Val Lys
 820 825 830

Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr Asp Gly Ser
 835 840 845

Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu Leu Gly Leu Gly
 850 855 860

Ser Asp Gly Gln Pro Pro Ala Gln Lys
 865 870

<210> 19

<211> 2622

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and *Rattus norvegicus*

<400> 19

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cgcattggtga ccgtcccccc acgccactac tgcattgtgg ccaacctgtg gtcccgggac	240
accagagtt ctgtgttatt tgacatcaca ggacaagtcc gactccggca cgctgaccag	300
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<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> completely synthesized

<400> 20.

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Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Pro Trp
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<210> 21

<211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 21
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<210> 22
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 22

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Pro

<210> 23
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 23
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<210> 24
 <211> 923
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 24

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 1 5 10 15

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Pro Met Ala

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Leu	Asp	Gln	Asn	Ser	Asn	Val	Ser	Arg	Val	Glu	Val	Gly	Pro	Lys	Thr
	50					55					60				
Tyr	Ile	Arg	Gln	Asp	Asn	Glu	Arg	Val	Leu	Phe	Ala	Pro	Met	Arg	Met
65					70					75					80
Val	Thr	Val	Pro	Pro	Arg	His	Tyr	Cys	Thr	Val	Ala	Asn	Pro	Val	Ser
				85					90					95	
Arg	Asp	Ala	Gln	Gly	Leu	Val	Leu	Phe	Asp	Val	Thr	Gly	Gln	Val	Arg
		100						105					110		
Leu	Arg	His	Ala	Asp	Leu	Glu	Ile	Arg	Leu	Ala	Gln	Asp	Pro	Phe	Pro
		115					120					125			
Leu	Tyr	Pro	Gly	Glu	Val	Leu	Glu	Lys	Asp	Ile	Thr	Pro	Leu	Gln	Val
	130					135					140				
Val	Leu	Pro	Asn	Thr	Ala	Leu	His	Leu	Lys	Ala	Leu	Leu	Asp	Phe	Glu
145					150					155					160
Asp	Lys	Asp	Gly	Asp	Lys	Val	Val	Ala	Gly	Asp	Glu	Trp	Leu	Phe	Glu
			165						170					175	
Gly	Pro	Gly	Thr	Tyr	Ile	Pro	Arg	Lys	Glu	Val	Glu	Val	Val	Glu	Ile
			180					185					190		
Ile	Gln	Ala	Thr	Ile	Ile	Arg	Gln	Asn	Gln	Ala	Leu	Arg	Leu	Arg	Ala
	195						200					205			
Arg	Lys	Glu	Cys	Trp	Asp	Arg	Asp	Gly	Lys	Glu	Arg	Val	Thr	Gly	Glu
	210					215					220				
Glu	Trp	Leu	Val	Thr	Thr	Val	Gly	Ala	Tyr	Leu	Pro	Ala	Val	Phe	Glu
225					230					235					240
Glu	Val	Leu	Asp	Leu	Val	Asp	Ala	Val	Ile	Leu	Thr	Glu	Lys	Thr	Ala
			245						250					255	

Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly Val Ser
 260 265 270

Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu Ala
 275 280 285

His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile Thr
 290 295 300

Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly Pro
 305 310 315 320

Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu Lys
 325 330 335

Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln Asp
 340 345 350

Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala Leu Gln
 355 360 365

Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln Ala Gly
 370 375 380

Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala Lys
 385 390 395 400

Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu Asn Glu
 405 410 415

Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val Ile
 420 425 430

Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys Glu
 435 440 445

Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp Pro Leu
 450 455 460

Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro Leu Ala
 465 470 475 480

Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn Ala
 485 490 495

Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val Val Phe
 500 505 510

Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr Val Leu
 515 520 525

Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala Leu
 530 535 540

Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile Glu
 545 550 555 560

Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp His
 565 570' 575

Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys Leu Phe
 580 585 590

Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser Arg
 595 600 605

Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys Asn
 610 615 620

Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr Ser Glu
 625 630 635 640

Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp Gln Ala
 645 650 655

Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln Ser
 660 665 670

Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser Val
 675 680 685

Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala Lys
 690 695 700

His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu Arg
 705 710 715 720

Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu Leu

725	730	735
Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly Thr Ala		
740	745	750
Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly Glu		
755	760	765
Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile Glu		
770	775	780
Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu Glu Leu		
785	790	795
Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln		
805	810	815
Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu Ala Ile		
820	825	830
Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met Gln		
835	840	845
Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr Asp		
850	855	860
Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu Leu Gly		
865	870	875
Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser Gly Pro		
885	890	895
Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro Gln Ala		
900	905	910
Pro Gly Asp Asn His Val Val Pro Val Leu Arg		
915	920	

<210> 25

<211> 2772

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 25
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 ccccatacc actatatcca tgtgctggac cagaacagca acgtgtcccg tgtggaggtc 180
 gggccaaaga cctacatccg gcaggacaat gagagggtac tgtttgcccc catgcgcatg 240
 gtgaccgtcc cccacgtca ctactgcaca gtggccaacc ctgtgtctcg ggatgccag 300
 ggcttgggtgc tgtttgatgt cacagggcaa gtccggcttc gccacgctga cctcgagatc 360
 cggctggccc aggaccctt cccctgtac ccaggggagg tgctggaaaa ggacatcaca 420
 cccctgcagg tggttctgcc caacactgcc ctccatctaa aggcgctgct tgattttgag 480
 gataaagatg gagacaaggt ggtggcagga gatgagtggc ttttcgaggg acctggcacg 540
 tacatcccc ggaaggaagt ggaggtcgtg gāgatcattc aggccaccat catcaggcag 600
 aaccaggctc tgcggctcag ggcccgcaag gagtgtctgg accgggacgg caaggagagg 660
 gtgacagggg aagaatggct ggtcaccaca gtaggggct acctcccagc ggtgtttgag 720
 gaggttctgg atttgggtga cgcgctcatc cttacggaaa agacagccct gcacctccgg 780
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 gtgcccata ccacctggg ccccccacaac tactgctga ttctcgacct tgtcggaccg 960
 gatggcaaga atcagctggg gcagaagcgc gtgggtcaagg gagagaagtc ttttttcctc 1020
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 taagactacc gagagaagcg agcccgctg gtcttcgggc ctgagctggt gtcgctgggt 1560
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ttccataaga actcagcccg catcattcgc actgctgtct ttggctttga gacctcgga 1920
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aacgggctgg tggtcagcag tgtggacgtg cagtcaagg agcctgtgga tcagaggacc 2040
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atggggcccg agggtcagcc cctgggcaga aggggtggcca gtggggccag ccctggggag 2700
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gtactgcgct aa 2772

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<210> 26

<211> 910

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 26

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Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1             5             10             15

```

```

Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
20             25             30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
35             40             45

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg

515	520	525
Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile		
530	535	540
Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr		
545	550	555
Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala		
565	570	575
Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile		
580	585	590
Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe		
595	600	605
His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu		
610	615	620
Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg		
625	630	635
Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp		
645	650	655
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln		
660	665	670
Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala		
675	680	685
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg		
690	695	700
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg		
705	710	715
Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr		
725	730	735
Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile		
740	745	750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu
 770 775 780

Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr
 805 810 815

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala
 865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
 885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg
 900 905 910

<210> 27

<211> 2733

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 27

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gaagagttca tcatccgcat cccccatac cactatatcc atgtgctgga ccagaacagc	120
aacgtgtccc gtgtggaggt cgggccaaag acctacatcc ggcaggacaa tgagagggtta	180
ctgtttgccc ccatgcgcat ggtgaccgtc cccccacgtc actactgcac agtggccaac	240
cctgtgtctc gggatgccca gggcttggtg ctgtttgatg tcacagggca agttcggctt	300

cgccacgctg	acctcgagat	ccggctggcc	caggaccctt	tccccctgta	cccaggggag	360
gtgctgga	aggacatcac	acccctgcag	gtggttctgc	ccaacactgc	cctccatcta	420
aaggcgctgc	ttgattttga	ggataaagat	ggagacaagg	tggtaggcagg	agatgagtgg	480
cttttcgagg	gacctggcac	gtacatcccc	cggaagggaag	tggaggctcg	ggagatcatt	540
caggccacca	tcatacaggca	gaaccaggct	ctgcggctca	gggcccgcga	ggagtgcctg	600
gaccgggacg	gcaaggagag	ggtgacaggg	gaagaatggc	tggtcaccac	agtaggggag	660
tacctccag	cggtgtttga	ggaggttctg	gatttggtgg	acgccgtcat	ccttacggaa	720
aagacagccc	tgcacctccg	ggctcggcgg	aacttccggg	acttcagggg	agtgtcccgc	780
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cacgaggagg	tgctgggggt	tgtgcccata	accaccctgg	gccccacaaa	ctactgcgtg	900
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gagaacgagg	gcatctatgt	gcaggatgtc	aagaccggaa	aggtgcgcgc	tgtgattgga	1260
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aagagcctcc	agcccttggc	gccccggaac	aagaccctg	tggtcagcta	ccgcgtgccc	1440
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cggcccaagc	gtcccatgc	ccgcctgctg	ctctgcctgc	tgtgggggcc	tgacttcttc	1620
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gcctctgtca	ctttcgatga	cttcataag	aactcagccc	gcatcattcg	cactgctgtc	1860
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gaccaggctg	tcttccccca	aaacgggctg	gtggtcagca	gtgtggacgt	gcagtcagtg	1980
gagcctgtgg	atcagaggac	ccgggacgcc	ctgcaacgca	gcgtccagct	ggccatcgag	2040

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atcaccacca actcccagga agcggcggcc aagcatgagg ctgagagact ggagcaggaa 2100
gcccgcgggc ggcttgagcg gcagaagatc ctggaccagt cagaagccga gaaagctcgc 2160
aaggaacttt tggagctgga ggctctgagc atggccgtgg agagcaccgg gactgccaag 2220
gcggaggccg agtcccgtgc ggaggcagcc cggattgagg gagaagggtc cgtgctgcag 2280
gccaaagctaa aagcacaggc cttggccatt gaaacggagg ctgagctcca gaggggtccag 2340
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gctcagcagc tggctgaggt ggaggtgaag aagttcaagc agatgacaga ggccataggc 2460
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agtggggcca gccctgggga ggggatatcc cccagtcctg ctcaggcccc tcaagctcct 2700
ggagacaacc acgtggtgcc tgtactgcgc taa 2733

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<210> 28
 <211> 892
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 28

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Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1           5           10           15

```

```

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Pro Trp Met
          20           25           30

```

```

Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His
          35           40           45

```

```

Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys
          50           55           60

```

```

Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg
          65           70           75           80

```

```

Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val
          85           90           95

```

Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val
 100 105 110

Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe
 115 120 125

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln
 130 135 140

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe
 145 150 155 160

Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe
 165 170 175

Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu
 180 185 190

Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg
 195 200 205

Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr Gly
 210 215 220

Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val Phe
 225 230 235 240

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr
 245 250 255

Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly Val
 260 265 270

Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu
 275 280 285

Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro Ile
 290 295 300

Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met Gly
 305 310 315 320

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu
 325 330 335

Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile Gln
 340 345 350

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala Leu
 355 360 365

Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln Ala
 370 375 380

Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala
 385 390 395 400

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln Asn
 405 410 415

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val
 420 425 430

Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys
 435 440 445

Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro
 450 455 460

Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser
 465 470 475 480

Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn
 485 490 495

Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val
 500 505 510

Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val
 515 520 525

Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala
 530 535 540

Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile
 545 550 555 560

Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp

	565		570		575														
His	Phe	Glu	Leu	Lys	Asn	Arg	Asn	Asp	Pro	Ala	Glu	Ala	Ala	Lys	Leu				
			580					585							590				
Phe	Ser	Val	Pro	Asp	Phe	Val	Gly	Asp	Ala	Cys	Lys	Ala	Ile	Ala	Ser				
			595				600					605							
Arg	Val	Arg	Gly	Ala	Val	Ala	Ser	Val	Thr	Phe	Asp	Asp	Phe	His	Lys				
			610			615					620								
Asn	Ser	Ala	Arg	Ile	Ile	Arg	Met	Ala	Val	Phe	Gly	Phe	Glu	Met	Ser				
625					630					635					640				
Glu	Asp	Thr	Gly	Pro	Asp	Gly	Thr	Leu	Leu	Pro	Lys	Ala	Arg	Asp	Gln				
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Ala	Val	Phe	Pro	Gln	Asn	Gly	Leu	Val	Val	Ser	Ser	Val	Asp	Val	Gln				
			660					665					670						
Ser	Val	Glu	Pro	Val	Asp	Gln	Arg	Thr	Arg	Asp	Ala	Leu	Gln	Arg	Ser				
			675				680						685						
Val	Gln	Leu	Ala	Ile	Glu	Ile	Thr	Thr	Asn	Ser	Gln	Glu	Ala	Ala	Ala				
			690			695					700								
Lys	His	Glu	Ala	Gln	Arg	Leu	Glu	Gln	Glu	Ala	Arg	Gly	Arg	Leu	Glu				
705					710					715					720				
Arg	Gln	Lys	Ile	Leu	Asp	Gln	Ser	Glu	Ala	Glu	Lys	Ala	Arg	Lys	Glu				
				725					730					735					
Leu	Leu	Glu	Leu	Glu	Ala	Met	Ser	Met	Ala	Val	Glu	Ser	Thr	Gly	Asn				
			740					745						750					
Ala	Lys	Ala	Glu	Ala	Glu	Ser	Arg	Ala	Glu	Ala	Ala	Arg	Ile	Glu	Gly				
			755				760						765						
Glu	Gly	Ser	Val	Leu	Gln	Ala	Lys	Leu	Lys	Ala	Gln	Ala	Leu	Ala	Ile				
			770			775					780								
Glu	Thr	Glu	Ala	Glu	Leu	Glu	Arg	Val	Lys	Lys	Val	Arg	Glu	Met	Glu				
785					790					795					800				

Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln
 805 810 815

Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu Ala
 820 825 830

Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met
 835 840 845

Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr
 850 855 860

Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu Leu
 865 870 875 880

Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
 885 890

<210> 29
 <211> 2679
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 29
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 atccccccat accactacat ccatgtgctg gaccagaaca gtaatgtgtc ccgtgtggag 180
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 atggtgaccg tccccccacg ccactactgc atagtggcca accctgtgtc cggggacacc 300
 cagagttctg tgttatttga catcacagga caagtccgac tccggcacgc tgaccaggag 360
 atccgactag cccaggaccc cttccccctg tatccagggg aggtgctgga aaaggacatc 420
 accccactgc aggtgggtct gcccaacaca gcactgcac ttaaggcggt gctggacttt 480
 gaggataaga atggagacaa ggtcatggca ggagacgagt ggctatttga gggacctggc 540
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 cgcgtagacag gtgaggagtgt gctgggtccga tccgtggggg cttacctccc agctgtcttt 720
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cgggctctgc agaacttcag ggaccttcgg ggagtgtccc accgcaccgg ggaggaatgg	840
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ccagacggca agaaccagct gggacaaaag cgtgttgtca agggagagaa gtcctttttc	1020
ctccagccag gagagaggct ggagcgaggc atccaggatg tgtatgtgct gtcagagcag	1080
caggggctgc tactgaaggc actgcagccc ctggaggagg gagagagcga ggagaaggtc	1140
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aaagtggagg tgggtggagga gcgtcaggct atccctctgg accaaaatga gggcatctat	1260
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caggatgaag tcctgtggga aaaggagctg ctttctgggg tggaggagct gctgaacttg	1380
gggcatgacc ctctggcaga caggggtcag aagggcacag ccaagcccct tcagccctca	1440
gctccaagga acaagacccg agtggtcagc tacogtgtcc cgcacaatgc agcgggtcag	1500
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gacgcctgca aggccattgc atcccagatc cggggggctg tagcctctgt cacctttgat	1860
gacttcata aaaactcagc ccggatcatt cgaatggctg tttttggctt tgagatgtct	1920
gaagacacag gtcctgatgg cacactcctg cccaaggctc gagaccaggc agtctttccc	1980
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ctgatctatg cccgggcccga gttggagctg gaggtgagca aggcgcagca gcttgccaat	2460
gtggaggcaa agaagttcaa ggagatgaca gaggcactgg gccccggcac catcagggac	2520

ctggctgtgg ccgggccaga gatgcaggtg aaacttctcc agtccctggg cctgaaatcc 2580
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 gggctggggg ctgatgggtca gccgccagca cagaagtga 2679

<210> 30
 <211> 878
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus
 <400> 30

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
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Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr
 20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val

165	170	175
Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg 180 185 190		
Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val 195 200 205		
Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala 210 215 220		
Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu 225 230 235 240		
Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg 245 250 255		
Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp 260 265 270		
Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val 275 280 285		
Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro 290 295 300		
Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys 305 310 315 320		
Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly 325 330 335		
Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys 340 345 350		
Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His 355 360 365		
Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro 370 375 380		
Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp 385 390 395 400		

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr
 725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu
 770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr
 805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys

865

870

875

<210> 31

<211> 2637

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and *Rattus norvegicus*

<400> 31

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aatgtgtccc gtgtggaggt tggaccaaag acctacatcc ggcaggacaa tgagagggta	180
ctgtttgccc cagttcgc atgtgaccgtc cccccacgcc actactgcat agtggccaac	240
cctgtgtccc gggacaccca gagttctgtg ttatttgaca tcacaggaca agtccgactc	300
cggcacgctg accaggagat ccgactagcc caggacccct tccccctgta tccaggggag	360
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aaggcgttgc tggactttga ggataagaat ggagacaagg tcatggcagg agacgagtgg	480
ctatttgagg gacctggcac ctacatccca cagaaggaag tggaaagtcgt ggagatcatt	540
caggccacag tcatcaaaca gaaccaagca ctgcggctaa gggcccgaaa ggagtgcctt	600
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tacctccag ctgtctttga agaggtgctg gatctggtgg atgctgtgat ccttacagaa	720
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gaggagctgc tgaacttggg gcatgaccct ctggcagaca ggggtcagaa gggcacagcc	1380

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tccttgggccc tgaaatccac tctcatcacc gatggctcgt ctcccatcaa cctcttcagc 2580
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<210> 32

<211> 96

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 32

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

<210> 33
 <211> 288
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 33
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 tgctccaaag aaaaaccgaa gtgcgccaag tgtctgaaga acaactggga gtgtcgctac 120
 tctcccaaaa ccaaagggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180
 ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240
 ttgaaaatgg attctttaca ggatataaaa gcattgttaa caggatta 288

<210> 34
 <211> 989
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> *Saccharomyces cerevisiae* and *Homo sapiens*

<400> 34

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
 1 5 10 15

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro

530	535	540
Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His		
545	550	555 560
Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val		
	565	570 575
Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr		
	580	585 590
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg		
	595	600 605
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr		
610	615	620
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn		
625	630	635 640
Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys		
	645	650 655
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala		
	660	665 670
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His		
	675	680 685
Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr		
690	695	700
Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp		
705	710	715 720
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val		
	725	730 735
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg		
	740	745 750
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala		
755	760	765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg
980 985

<210> 35
<211> 2970

<212> DNA

<213> Artificial Sequence

<220>

<223> *Saccharomyces cerevisiae* and *Homo sapiens*

<400> 35

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gagttcatca tccgcatccc ccataccac tatatccatg tgctggacca gaacagcaac	360
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<210> 36

<211> 957

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccharomyces cerevisiae* and *Rattus norvegicus*

<400> 36

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

465	470	475	480
Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala	485	490	495
Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu	500	505	510
Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp	515	520	525
Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro	530	535	540
Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His	545	550	555
Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val	565	570	575
Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr	580	585	590
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg	595	600	605
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr	610	615	620
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn	625	630	635
Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys	645	650	655
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala	660	665	670
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His	675	680	685
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met	690	695	700

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
 945 950 955

<210> 37
 <211> 2874
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Saccharomyces cerevisiae* and *Rattus norvegicus*

<400> 37
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 ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240
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<210> 38
 <211> 130
 <212> PRT
 <213> Levivirus

<400> 38

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
 1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr
 130

<210> 39
 <211> 393
 <212> DNA
 <213> Levivirus

<400> 39
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 tcagcaatcg cagcaaactc cggcatctac ccc 393

<210> 40
 <211> 1024
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens

<400> 40

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
 1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr
 130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
 165 170 175

Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val
 180 185 190

Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val
 195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala
 210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
 225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
 245 250 255

Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp
 260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp
 355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu
 435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val
 530 535 540

Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys
 545 550 555 560

Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser
 565 570 575

Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu
 610 615 620

Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His
 625 630 635 640

Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp
 645 650 655

Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu

660	665	670
Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu		
675	680	685
Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys		
690	695	700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp		
705	710	715
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly		
725	730	735
Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg		
740	745	750
Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser		
755	760	765
Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala		
770	775	780
Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln		
785	790	795
Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg		
805	810	815
Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys		
820	825	830
Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu		
835	840	845
Ser Thr Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala		
850	855	860
Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln		
865	870	875
Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val		
885	890	895

Arg Glu Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln
 915 920 925

Met Thr Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala
 965 970 975

Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg
 980 985 990

Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala
 995 1000 1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu
 1010 1015 1020

Arg

<210> 41
 <211> 3075
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens

<400> 41
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 caggcttaca aagtaacctg tagcgttcgt cagagctctg cgcagaatcg caaatacacc 180
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 tcagcaatcg cagcaaactc cggcatctac cccatggcaa ctgaagagtt catcatccgc 420

atccccccat accactatat ccatgtgctg gaccagaaca gcaacgtgtc ccgtgtggag	480
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caggggctgc tgctgagggc cctgcagccc ctggaggagg gggaggatga ggagaaggtc	1440
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aaagtggagg tgggtggagga gcgccaggcc atccctctag acgagaacga gggcatctat	1560
gtgcaggatg tcaagaccgg aaaggtgcgc gctgtgattg gaagcaccta catgctgacc	1620
caggacgaag tcctgtggga gaaagagctg cctccccggg tggaggagct gctgaacaag	1680
gggcaggacc ctctggcaga caggggtgag aaggacacag ctaagagcct ccagcccttg	1740
gogccccgga acaagaccg tgtggtcagc taccgctgc cccacaacgc tgcggtgcag	1800
gtgtacgact accgagagaa gcgagcccgc gtggtcttcg ggcttgagct ggtgtcgtg	1860
ggtcctgagg agcagttcac agtggtgtcc ctctcagctg ggcggcccaa gcgtcccat	1920
gcccgcctg cgctctgcct gctgctgggg cctgacttct tcacagacgt catcaccatc	1980
gaaacggcgg atcatgccag gctgcaactg cagctggcct acaactggca ctttgagggt	2040
aatgaccgga aggaccccca agagacggcc aagctctttt cagtgccaga ctttgtaggt	2100
gatgcctgca aagccatcgc atcccggtg cggggggccg tggcctctgt cactttcgat	2160

```

gacttccata agaactcagc ccgcatcatt cgcactgctg tctttggctt tgagacctcg 2220
gaagcgaagg gccccgatgg catggccctg cccaggcccc gggaccaggc tgtcttcccc 2280
caaaacgggc tgggtggtcag cagtgtggac gtgcagtcag tggagcctgt ggatcagagg 2340
acccgggacg ccctgcaacg cagcgtccag ctggccatcg agatcaccac caactcccag 2400
gaagcggcgg ccaagcatga ggctcagaga ctggagcagg aagcccgcgg ccggcttgag 2460
cggcagaaga tcctggacca gtcagaagcc gagaaagctc gcaaggaact tttggagctg 2520
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ctggctctatg cccgggcccc gctggagctg gaggtgagca aggctcagca gctggctgag 2760
gtggagggtga agaagttcaa gcagatgaca gaggccatag gcccagcac catcagggac 2820
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gggatggggc ccgaggggtca gccctggggc agaaggggtg ccagtgggac cagccctggg 3000
gaggggatat ccccccagtc tgctcaggcc cctcaagctc ctggagacaa ccacgtggtg 3060
cctgtactgc gctaa 3075

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<210> 42
 <211> 992
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Levivirus and Rattus norvegicus

<400> 42

```

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1           5           10          15

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```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
          20          25          30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
          35          40          45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
          50          55          60

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr
130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val
180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile
195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala
210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp
260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val
275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala
290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val

530		535		540
Leu Trp Glu Lys Glu	Leu Pro Ser Gly Val	Glu Glu Leu Leu Asn Leu		
545	550	555		560
Gly His Asp Pro Leu	Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro			
	565	570		575
Leu Gln Pro Ser Ala Pro	Arg Asn Lys Thr Arg Val Val Ser Tyr Arg			
	580	585		590
Val Pro His Asn Ala Ala Val	Gln Val Tyr Asp Tyr Arg Ala Lys Arg			
	595	600		605
Ala Arg Val Val Phe Gly	Pro Glu Leu Val Thr Leu Asp Pro Glu Glu			
	610	615		620
Gln Phe Thr Val Leu Ser	Leu Ser Ala Gly Arg Pro Lys Arg Pro His			
	625	630		635
Ala Arg Arg Ala Leu Cys	Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp			
	645	650		655
Val Ile Thr Ile Glu Thr	Ala Asp His Ala Arg Leu Gln Leu Gln Leu			
	660	665		670
Ala Tyr Asn Trp His Phe	Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu			
	675	680		685
Ala Ala Lys Leu Phe Ser	Val Pro Asp Phe Val Gly Asp Ala Cys Lys			
	690	695		700
Ala Ile Ala Ser Arg Val	Arg Gly Ala Val Ala Ser Val Thr Phe Asp			
	705	710		715
Asp Phe His Lys Asn Ser	Ala Arg Ile Ile Arg Met Ala Val Phe Gly			
	725	730		735
Phe Glu Met Ser Glu Asp	Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys			
	740	745		750
Ala Arg Asp Gln Ala Val	Phe Pro Gln Asn Gly Leu Val Val Ser Ser			
	755	760		765

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala
 770 775 780
 Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln
 785 790 795 800
 Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg
 805 810 815
 Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys
 820 825 830
 Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu
 835 840 845
 Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala
 850 855 860
 Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln
 865 870 875 880
 Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val
 885 890 895
 Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
 900 905 910
 Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu
 915 920 925
 Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala
 930 935 940
 Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 945 950 955 960
 Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala
 965 970 975
 Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
 980 985 990

<210> 43
 <211> 2979

<212> DNA

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus

<400> 43

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gtcgcccca gcaacttcgc taacgggggtc gctgaatgga tcagctctaa ctgcggttca	120
caggcttaca aagtaacctg tagcgttcgt cagagctctg cgcagaatcg caaatacacc	180
atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtgggtgtaga gcttcctgta	240
gccgcatggc gttcgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc	300
gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc	360
tcagcaatcg cagcaaactc cggcattctac cccatggcaa ctgaagaggc catcatccgc	420
atcccccat accactacat ccatgtgctg gaccagaaca gtaatgtgtc ccgtgtggag	480
gttggaacaa agacctacat ccggcaggac aatgagaggg tactgtttgc ccagttcgc	540
atggtgaccg tccccccacg ccactactgc atagtggcca accctgtgtc ccgggacacc	600
cagagttctg tgttatttga catcacagga caagtccgac tccggcacgc tgaccaggag	660
atccgactag ccaggagccc cttccccctg tatccagggg aggtgctgga aaaggacatc	720
acccactgc aggtggttct gcccaacaca gcactgcac ttaaggcggt gctggacttt	780
gaggataaga atggagacaa ggtcatggca ggagacgagt ggctatttga gggacctggc	840
acctacatcc cacagaagga agtggaaagtc gtggagatca ttcaggccac agtcatcaaa	900
cagaaccaag cactgcggct aaggggcccga aaggagtgtc ttgaccggga gggcaagggg	960
cgcgtagacag gtgaggagtg gctgggtccga tccgtggggg cttacctccc agctgtcttt	1020
gaagaggtgc tggatctggt ggatgctgtg atccttacag aaaagactgc cctgcacctc	1080
cgggctctgc agaacttcag ggaccttcgg ggagtgtcc accgcaccgg ggaggaatgg	1140
ttagtacag tgcaggacac agaagcccat gttccagatg tctatgagga ggtgcttggg	1200
gtagtaccca tcaccaccct gggacctcga cactactgtg tcattcttga cccaatggga	1260
ccagacggca agaaccagct gggacaaaag cgtgttgtca agggagagaa gtcctttttc	1320
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caggggctgc tactgaaggc actgcagccc ctggaggagg gagagagcga ggagaaggtc	1440
tcccatcagg ccggagactg ctggctcatc cgtgggcccc tggagtatgt gccatctgca	1500
aaagtggagg tgggtggagga gcgtcaggct atccctctgg accaaaatga gggcatctat	1560

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gtgcaggatg tcaagacggg gaaggtgcgg gctgtgattg gaagcaccta catgctgact 1620
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gggcatgacc ctctggcaga caggggtcag aagggcacag ccaagcccct tcagccctca 1740
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gaaactgcag atcatgccag gttgcagctg cagcttgctt acaactggca ctttgaactg 2040
aagaaccgga atgaccctgc agaggcagcc aagcttttct cctgcctga cttcgtgggt 2100
gacgcctgca aggccattgc atcccagctc cggggggctg tagcctctgt cacctttgat 2160
gacttcata aaaactcagc ccggatcatt cgaatggctg tttttggctt tgagatgtct 2220
gaagacacag gtcctgatgg cacactcctg cccaaggctc gagaccaggc agtctttccc 2280
caaaacgggc tggtagtcag cagtgtggat gtgcagtcag tggagcccgt ggaccagagg 2340
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gtggaggcaa agaagttcaa ggagatgaca gaggcactgg gcccggcac catcagggac 2820
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actctcatca ccgatggctc gtctcccatc aacctcttca gcacagcctt cgggttgctg 2940
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<210> 44

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> completely synthesized

<400> 44

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro
 225 230 235

<210> 45
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 45
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 gatgtgaatg ggcacaaatt ttctgtcagc ggagaggggtg aaggtgatgc cacatacggg 120
 aagctcaccg tgaaattcat ctgcaccact ggaaagctcc ctgtgccatg gccaacactg 180
 gtcactacct tcacctatgg cgtgcagtgc ttttccagat acccagacca tatgaagcag 240
 catgactttt tcaagagcgc catgcccagag ggctatgtgc aggagagaac catctttttc 300
 aaagatgacg ggaactacaa gaccgcgcgt gaagtcaagt tcgaagggtga caccctgggtg 360
 aatagaatcg agctgaaggg cattgacttt aaggaggatg gaaacattct cggccacaag 420
 ctggaataca actataactc ccacaatgtg tacatcatgg ccgacaagca aaagaatggc 480
 atcaagggtca acttcaagat cagacacaac attgaggatg gatccgtgca gctggccgac 540
 cattatcaac agaacactcc aatcgggcgc ggccctgtgc tcctcccaga caaccattac 600
 ctgtccaccc agtctgccct gtctaaagat cccaacgaaa agagagacca catgggtcctg 660
 ctggagtttg tgaccgctgc tgggatcaca catggcatgg acgagctgta caagcccatg 720

<210> 46
 <211> 1132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 46

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

50																	
Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln		
65					70					75					80		
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
				85					90					95			
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
			100					105						110			
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
		115					120					125					
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
	130					135					140						
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
145					150					155					160		
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		
			165						170					175			
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro		
			180					185					190				
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser		
		195					200					205					
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val		
	210					215					220						
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Pro	Met		
225					230					235					240		
Ala	Thr	Glu	Glu	Phe	Ile	Ile	Arg	Ile	Pro	Pro	Tyr	His	Tyr	Ile	His		
				245					250					255			
Val	Leu	Asp	Gln	Asn	Ser	Asn	Val	Ser	Arg	Val	Glu	Val	Gly	Pro	Lys		
			260					265					270				
Thr	Tyr	Ile	Arg	Gln	Asp	Asn	Glu	Arg	Val	Leu	Phe	Ala	Pro	Met	Arg		
		275					280					285					

Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro Val
 290 295 300

Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln Val
 305 310 315 320

Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro Phe
 325 330 335

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln
 340 345 350

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe
 355 360 365

Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu Phe
 370 375 380

Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val Glu
 385 390 395 400

Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu Arg
 405 410 415

Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr Gly
 420 425 430

Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val Phe
 435 440 445

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr
 450 455 460

Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly Val
 465 470 475 480

Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu
 485 490 495

Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile
 500 505 510

Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly
 515 520 525

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu
 530 535 540

Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln
 545 550 555 560

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala Leu
 565 570 575

Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln Ala
 580 585 590

Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala
 595 600 605

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu Asn
 610 615 620

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val
 625 630 635 640

Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys
 645 650 655

Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp Pro
 660 665 670

Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro Leu
 675 680 685

Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn
 690 695 700

Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val Val
 705 710 715 720

Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr Val
 725 730 735

Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala
 740 745 750

Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile

755	760	765
Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp 770 775 780		
His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys Leu 785 790 795 800		
Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser 805 810 815		
Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys 820 825 830		
Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr Ser 835 840 845		
Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp Gln 850 855 860		
Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln 865 870 875 880		
Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser 885 890 895		
Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala 900 905 910		
Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu 915 920 925		
Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu 930 935 940		
Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly Thr 945 950 955 960		
Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly 965 970 975		
Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile 980 985 990		

Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu Glu
 995 1000 1005

Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 1010 1015 1020

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr
 1025 1030 1035

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly
 1040 1045 1050

Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 1055 1060 1065

Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr
 1070 1075 1080

Ala Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly
 1085 1090 1095

Arg Arg Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro
 1100 1105 1110

Gln Ser Ala Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val
 1115 1120 1125

Pro Val Leu Arg
 1130

<210> 47
 <211> 3399
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 47

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Ala Ala Cys Thr Gly Thr Thr Cys Ala Cys Thr Gly Gly Cys Gly Thr
 20 25 30

Gly Gly Thr Cys Cys Cys Ala Ala Thr Thr Cys Thr Cys Gly Thr Gly
 35 40 45

Gly Ala Ala Cys Thr Gly Gly Ala Thr Gly Gly Cys Gly Ala Thr Gly
 50 55 60

Thr Gly Ala Ala Thr Gly Gly Gly Cys Ala Cys Ala Ala Ala Thr Thr
 65 70 75 80

Thr Thr Cys Thr Gly Thr Cys Ala Gly Cys Gly Gly Ala Gly Ala Gly
 85 90 95

Gly Gly Thr Gly Ala Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Ala
 100 105 110

Cys Ala Thr Ala Cys Gly Gly Ala Ala Ala Gly Cys Thr Cys Ala Cys
 115 120 125

Cys Cys Thr Gly Ala Ala Ala Thr Thr Cys Ala Thr Cys Thr Gly Cys
 130 135 140

Ala Cys Cys Ala Cys Thr Gly Gly Ala Ala Ala Gly Cys Thr Cys Cys
 145 150 155 160

Cys Thr Gly Thr Gly Cys Cys Ala Thr Gly Gly Cys Cys Ala Ala Cys
 165 170 175

Ala Cys Thr Gly Gly Thr Cys Ala Cys Thr Ala Cys Cys Thr Thr Cys
 180 185 190

Ala Cys Cys Thr Ala Thr Gly Gly Cys Gly Thr Gly Cys Ala Gly Thr
 195 200 205

Gly Cys Thr Thr Thr Thr Cys Cys Ala Gly Ala Thr Ala Cys Cys Cys
 210 215 220

Ala Gly Ala Cys Cys Ala Thr Ala Thr Gly Ala Ala Gly Cys Ala Gly
 225 230 235 240

Cys Ala Thr Gly Ala Cys Thr Thr Thr Thr Thr Cys Ala Ala Gly Ala
 245 250 255

Gly Cys Gly Cys Cys Ala Thr Gly Cys Cys Cys Gly Ala Gly Gly Gly
 260 265 270

Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Gly Ala Gly Ala
 275 280 285

Ala Cys Cys Ala Thr Cys Thr Thr Thr Thr Thr Cys Ala Ala Ala Gly
 290 295 300

Ala Thr Gly Ala Cys Gly Gly Gly Ala Ala Cys Thr Ala Cys Ala Ala
 305 310 315 320

Gly Ala Cys Cys Cys Gly Cys Gly Cys Thr Gly Ala Ala Gly Thr Cys
 325 330 335

Ala Ala Gly Thr Thr Cys Gly Ala Ala Gly Gly Thr Gly Ala Cys Ala
 340 345 350

Cys Cys Cys Thr Gly Gly Thr Gly Ala Ala Thr Ala Gly Ala Ala Thr
 355 360 365

Cys Gly Ala Gly Cys Thr Gly Ala Ala Gly Gly Gly Cys Ala Thr Thr
 370 375 380

Gly Ala Cys Thr Thr Thr Ala Ala Gly Gly Ala Gly Gly Ala Thr Gly
 385 390 395 400

Gly Ala Ala Ala Cys Ala Thr Thr Cys Thr Cys Gly Gly Cys Cys Ala
 405 410 415

Cys Ala Ala Gly Cys Thr Gly Gly Ala Ala Thr Ala Cys Ala Ala Cys
 420 425 430

Thr Ala Thr Ala Ala Cys Thr Cys Cys Cys Ala Cys Ala Ala Thr Gly
 435 440 445

Thr Gly Thr Ala Cys Ala Thr Cys Ala Thr Gly Gly Cys Cys Gly Ala
 450 455 460

Cys Ala Ala Gly Cys Ala Ala Ala Ala Gly Ala Ala Thr Gly Gly Cys
 465 470 475 480

Ala Thr Cys Ala Ala Gly Gly Thr Cys Ala Ala Cys Thr Thr Cys Ala
 485 490 495

Ala Gly Ala Thr Cys Ala Gly Ala Cys Ala Cys Ala Ala Cys Ala Thr

500	505	510
Thr Gly Ala Gly Gly Ala	Thr Gly Gly Ala Thr	Cys Cys Gly Thr Gly
515	520	525
Cys Ala Gly Cys Thr Gly	Gly Cys Cys Gly Ala	Cys Cys Ala Thr Thr
530	535	540
Ala Thr Cys Ala Ala Cys	Ala Gly Ala Ala Cys	Ala Cys Thr Cys Cys
545	550	555
Ala Ala Thr Cys Gly Gly	Cys Gly Ala Cys Gly	Cys Cys Cys Thr
565	570	575
Gly Thr Gly Cys Thr Cys	Cys Cys Thr Cys Cys	Ala Gly Ala Cys Ala
580	585	590
Ala Cys Cys Ala Thr Thr	Ala Cys Cys Thr Gly	Thr Cys Cys Ala Cys
595	600	605
Cys Cys Ala Gly Thr Cys	Thr Gly Cys Cys Cys	Thr Gly Thr Cys Thr
610	615	620
Ala Ala Ala Gly Ala Thr	Cys Cys Cys Ala Ala	Cys Gly Ala Ala Ala
625	630	635
Ala Gly Ala Gly Ala Gly	Ala Cys Cys Ala Cys	Ala Thr Gly Gly Thr
645	650	655
Cys Cys Thr Gly Cys Thr	Gly Gly Ala Gly Thr	Thr Thr Thr Gly Thr
660	665	670
Ala Cys Cys Gly Cys Thr	Gly Cys Thr Gly Gly	Gly Ala Thr Cys Ala
675	680	685
Cys Ala Cys Ala Thr Gly	Gly Cys Ala Thr Gly	Gly Ala Cys Gly Ala
690	695	700
Gly Cys Thr Gly Thr Ala	Cys Ala Ala Gly Cys	Cys Cys Ala Thr Gly
705	710	715
Gly Cys Ala Ala Cys Thr	Gly Ala Ala Gly Thr	Thr Cys Ala
725	730	735

Thr Cys Ala Thr Cys Cys Gly Cys Ala Thr Cys Cys Cys Cys Cys Cys
 740 745 750

Ala Thr Ala Cys Cys Ala Cys Thr Ala Thr Ala Thr Cys Cys Ala Thr
 755 760 765

Gly Thr Gly Cys Thr Gly Gly Ala Cys Cys Ala Gly Ala Ala Cys Ala
 770 775 780

Gly Cys Ala Ala Cys Gly Thr Gly Thr Cys Cys Cys Gly Thr Gly Thr
 785 790 795 800

Gly Gly Ala Gly Gly Thr Cys Gly Gly Gly Cys Cys Ala Ala Ala Gly
 805 810 815

Ala Cys Cys Thr Ala Cys Ala Thr Cys Cys Gly Gly Cys Ala Gly Gly
 820 825 830

Ala Cys Ala Ala Thr Gly Ala Gly Ala Gly Gly Gly Thr Ala Cys Thr
 835 840 845

Gly Thr Thr Thr Gly Cys Cys Cys Cys Cys Ala Thr Gly Cys Gly Cys
 850 855 860

Ala Thr Gly Gly Thr Gly Ala Cys Cys Gly Thr Cys Cys Cys Cys Cys
 865 870 875 880

Cys Ala Cys Gly Thr Cys Ala Cys Thr Ala Cys Thr Gly Cys Ala Cys
 885 890 895

Ala Gly Thr Gly Gly Cys Cys Ala Ala Cys Cys Cys Thr Gly Thr Gly
 900 905 910

Thr Cys Thr Cys Gly Gly Gly Ala Thr Gly Cys Cys Cys Ala Gly Gly
 915 920 925

Gly Cys Thr Thr Gly Gly Thr Gly Cys Thr Gly Thr Thr Thr Gly Ala
 930 935 940

Thr Gly Thr Cys Ala Cys Ala Gly Gly Gly Cys Ala Ala Gly Thr Thr
 945 950 955 960

Cys Gly Gly Cys Thr Thr Cys Gly Cys Cys Ala Cys Gly Cys Thr Gly
 965 970 975

Ala Cys Cys Thr Cys Gly Ala Gly Ala Thr Cys Cys Gly Gly Cys Thr
 980 985 990

Gly Gly Cys Cys Cys Ala Gly Gly Ala Cys Cys Cys Cys Thr Thr Cys
 995 1000 1005

Cys Cys Cys Cys Thr Gly Thr Ala Cys Cys Cys Ala Gly Gly Gly
 1010 1015 1020

Gly Ala Gly Gly Thr Gly Cys Thr Gly Gly Ala Ala Ala Ala Gly
 1025 1030 1035

Gly Ala Cys Ala Thr Cys Ala Cys Ala Cys Cys Cys Cys Thr Gly
 1040 1045 1050

Cys Ala Gly Gly Thr Gly Gly Thr Thr Cys Thr Gly Cys Cys Cys
 1055 1060 1065

Ala Ala Cys Ala Cys Thr Gly Cys Cys Cys Thr Cys Cys Ala Thr
 1070 1075 1080

Cys Thr Ala Ala Ala Gly Gly Cys Gly Cys Thr Gly Cys Thr Thr
 1085 1090 1095

Gly Ala Thr Thr Thr Thr Gly Ala Gly Gly Ala Thr Ala Ala Ala
 1100 1105 1110

Gly Ala Thr Gly Gly Ala Gly Ala Cys Ala Ala Gly Gly Thr Gly
 1115 1120 1125

Gly Thr Gly Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Ala Gly
 1130 1135 1140

Thr Gly Gly Cys Thr Thr Thr Thr Cys Gly Ala Gly Gly Gly Ala
 1145 1150 1155

Cys Cys Thr Gly Gly Cys Ala Cys Gly Thr Ala Cys Ala Thr Cys
 1160 1165 1170

Cys Cys Cys Cys Gly Gly Ala Ala Gly Gly Ala Ala Gly Thr Gly
 1175 1180 1185

Gly Ala Gly Gly Thr Cys Gly Thr Gly Gly Ala Gly Ala Thr Cys

1190	1195	1200
Ala Thr Thr Cys Ala Gly Gly Cys Cys Ala Cys Cys Ala Thr Cys 1205 1210 1215		
Ala Thr Cys Ala Gly Gly Cys Ala Gly Ala Ala Cys Cys Ala Gly 1220 1225 1230		
Gly Cys Thr Cys Thr Gly Cys Gly Gly Cys Thr Cys Ala Gly Gly 1235 1240 1245		
Gly Cys Cys Cys Gly Cys Ala Ala Gly Gly Ala Gly Thr Gly Cys 1250 1255 1260		
Thr Gly Gly Gly Ala Cys Cys Gly Gly Gly Ala Cys Gly Gly Cys 1265 1270 1275		
Ala Ala Gly Gly Ala Gly Ala Gly Gly Gly Thr Gly Ala Cys Ala 1280 1285 1290		
Gly Gly Gly Gly Ala Ala Gly Ala Ala Thr Gly Gly Cys Thr Gly 1295 1300 1305		
Gly Thr Cys Ala Cys Cys Ala Cys Ala Gly Thr Ala Gly Gly Gly 1310 1315 1320		
Gly Cys Gly Thr Ala Cys Cys Thr Cys Cys Cys Ala Gly Cys Gly 1325 1330 1335		
Gly Thr Gly Thr Thr Thr Gly Ala Gly Gly Ala Gly Gly Thr Thr 1340 1345 1350		
Cys Thr Gly Gly Ala Thr Thr Thr Gly Gly Thr Gly Gly Ala Cys 1355 1360 1365		
Gly Cys Cys Gly Thr Cys Ala Thr Cys Cys Thr Thr Ala Cys Gly 1370 1375 1380		
Gly Ala Ala Ala Ala Gly Ala Cys Ala Gly Cys Cys Cys Thr Gly 1385 1390 1395		
Cys Ala Cys Cys Thr Cys Cys Gly Gly Gly Cys Thr Cys Gly Gly 1400 1405 1410		

Cys Gly Gly Ala Ala Cys Thr Thr Cys Cys Gly Gly Gly Ala Cys
 1415 1420 1425

Thr Thr Cys Ala Gly Gly Gly Gly Ala Gly Thr Gly Thr Cys Cys
 1430 1435 1440

Cys Gly Cys Cys Gly Cys Ala Cys Thr Gly Gly Gly Gly Ala Gly
 1445 1450 1455

Gly Ala Gly Thr Gly Gly Cys Thr Gly Gly Thr Ala Ala Cys Ala
 1460 1465 1470

Gly Thr Gly Cys Ala Gly Gly Ala Cys Ala Cys Ala Gly Ala Gly
 1475 1480 1485

Gly Cys Cys Cys Ala Cys Gly Thr Gly Cys Cys Ala Gly Ala Thr
 1490 1495 1500

Gly Thr Cys Cys Ala Cys Gly Ala Gly Gly Ala Gly Gly Thr Gly
 1505 1510 1515

Cys Thr Gly Gly Gly Gly Gly Thr Thr Gly Thr Gly Cys Cys Cys
 1520 1525 1530

Ala Thr Cys Ala Cys Cys Ala Cys Cys Cys Thr Gly Gly Gly Cys
 1535 1540 1545

Cys Cys Cys Cys Ala Cys Ala Ala Cys Thr Ala Cys Thr Gly Cys
 1550 1555 1560

Gly Thr Gly Ala Thr Thr Cys Thr Cys Gly Ala Cys Cys Cys Thr
 1565 1570 1575

Gly Thr Cys Gly Gly Ala Cys Cys Gly Gly Ala Thr Gly Gly Cys
 1580 1585 1590

Ala Ala Gly Ala Ala Thr Cys Ala Gly Cys Thr Gly Gly Gly Gly
 1595 1600 1605

Cys Ala Gly Ala Ala Gly Cys Gly Cys Gly Thr Gly Gly Thr Cys
 1610 1615 1620

Ala Ala Gly Gly Gly Ala Gly Ala Gly Ala Ala Gly Thr Cys Thr
 1625 1630 1635

Thr Thr Thr Thr Thr Cys Cys Thr Cys Cys Ala Gly Cys Cys Ala
 1640 1645 1650

Gly Gly Ala Gly Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala
 1655 1660 1665

Cys Ala Ala Gly Gly Cys Ala Thr Cys Cys Ala Gly Gly Ala Thr
 1670 1675 1680

Gly Thr Gly Thr Ala Thr Gly Thr Gly Cys Thr Gly Thr Cys Gly
 1685 1690 1695

Gly Ala Gly Cys Ala Gly Cys Ala Gly Gly Gly Gly Cys Thr Gly
 1700 1705 1710

Cys Thr Gly Cys Thr Gly Ala Gly Gly Gly Cys Cys Cys Thr Gly
 1715 1720 1725

Cys Ala Gly Cys Cys Cys Cys Thr Gly Gly Ala Gly Gly Ala Gly
 1730 1735 1740

Gly Gly Gly Gly Ala Gly Gly Ala Thr Gly Ala Gly Gly Ala Gly
 1745 1750 1755

Ala Ala Gly Gly Thr Cys Thr Cys Ala Cys Ala Cys Cys Ala Gly
 1760 1765 1770

Gly Cys Thr Gly Gly Gly Gly Ala Cys Cys Ala Cys Thr Gly Gly
 1775 1780 1785

Cys Thr Cys Ala Thr Cys Cys Gly Cys Gly Gly Ala Cys Cys Cys
 1790 1795 1800

Cys Thr Gly Gly Ala Gly Thr Ala Thr Gly Thr Gly Cys Cys Ala
 1805 1810 1815

Thr Cys Thr Gly Cys Cys Ala Ala Ala Gly Thr Gly Gly Ala Gly
 1820 1825 1830

Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Gly Cys
 1835 1840 1845

Cys Ala Gly Gly Cys Cys Ala Thr Cys Cys Cys Thr Cys Thr Ala

1850		1855		1860
Gly Ala Cys Gly Ala Gly Ala Ala Cys Gly Ala Gly Gly Gly Cys				
1865		1870		1875
Ala Thr Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Thr				
1880		1885		1890
Gly Thr Cys Ala Ala Gly Ala Cys Cys Gly Gly Ala Ala Ala Gly				
1895		1900		1905
Gly Thr Gly Cys Gly Cys Gly Cys Thr Gly Thr Gly Ala Thr Thr				
1910		1915		1920
Gly Gly Ala Ala Gly Cys Ala Cys Cys Thr Ala Cys Ala Thr Gly				
1925		1930		1935
Cys Thr Gly Ala Cys Cys Cys Ala Gly Gly Ala Cys Gly Ala Ala				
1940		1945		1950
Gly Thr Cys Cys Thr Gly Thr Gly Gly Gly Ala Gly Ala Ala Ala				
1955		1960		1965
Gly Ala Gly Cys Thr Gly Cys Cys Thr Cys Cys Cys Gly Gly Gly				
1970		1975		1980
Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Thr Gly Cys Thr Gly				
1985		1990		1995
Ala Ala Cys Ala Ala Gly Gly Gly Gly Cys Ala Gly Gly Ala Cys				
2000		2005		2010
Cys Cys Thr Cys Thr Gly Gly Cys Ala Gly Ala Cys Ala Gly Gly				
2015		2020		2025
Gly Gly Thr Gly Ala Gly Ala Ala Gly Gly Ala Cys Ala Cys Ala				
2030		2035		2040
Gly Cys Thr Ala Ala Gly Ala Gly Cys Cys Thr Cys Cys Ala Gly				
2045		2050		2055
Cys Cys Cys Thr Thr Gly Gly Cys Gly Cys Cys Cys Cys Gly Gly				
2060		2065		2070

Ala Ala Cys Ala Ala Gly Ala Cys Cys Cys Gly Thr Gly Thr Gly		
2075	2080	2085
Gly Thr Cys Ala Gly Cys Thr Ala Cys Cys Gly Cys Gly Thr Gly		
2090	2095	2100
Cys Cys Cys Cys Ala Cys Ala Ala Cys Gly Cys Thr Gly Cys Gly		
2105	2110	2115
Gly Thr Gly Cys Ala Gly Gly Thr Gly Thr Ala Cys Gly Ala Cys		
2120	2125	2130
Thr Ala Cys Cys Gly Ala Gly Ala Gly Ala Ala Gly Cys Gly Ala		
2135	2140	2145
Gly Cys Cys Cys Gly Cys Gly Thr Gly Gly Thr Cys Thr Thr Cys		
2150	2155	2160
Gly Gly Gly Cys Cys Thr Gly Ala Gly Cys Thr Gly Gly Thr Gly		
2165	2170	2175
Thr Cys Gly Cys Thr Gly Gly Gly Thr Cys Cys Thr Gly Ala Gly		
2180	2185	2190
Gly Ala Gly Cys Ala Gly Thr Thr Cys Ala Cys Ala Gly Thr Gly		
2195	2200	2205
Thr Thr Gly Thr Cys Cys Cys Thr Cys Thr Cys Ala Gly Cys Thr		
2210	2215	2220
Gly Gly Gly Cys Gly Gly Cys Cys Cys Ala Ala Gly Cys Gly Thr		
2225	2230	2235
Cys Cys Cys Cys Ala Thr Gly Cys Cys Cys Gly Cys Cys Gly Thr		
2240	2245	2250
Gly Cys Gly Cys Thr Cys Thr Gly Cys Cys Thr Gly Cys Thr Gly		
2255	2260	2265
Cys Thr Gly Gly Gly Gly Cys Cys Thr Gly Ala Cys Thr Thr Cys		
2270	2275	2280
Thr Thr Cys Ala Cys Ala Gly Ala Cys Gly Thr Cys Ala Thr Cys		
2285	2290	2295

Ala Cys Cys Ala Thr Cys Gly Ala Ala Ala Cys Gly Gly Cys Gly
 2300 2305 2310

Gly Ala Thr Cys Ala Thr Gly Cys Cys Ala Gly Gly Cys Thr Gly
 2315 2320 2325

Cys Ala Ala Cys Thr Gly Cys Ala Gly Cys Thr Gly Gly Cys Cys
 2330 2335 2340

Thr Ala Cys Ala Ala Cys Thr Gly Gly Cys Ala Cys Thr Thr Thr
 2345 2350 2355

Gly Ala Gly Gly Thr Gly Ala Ala Thr Gly Ala Cys Cys Gly Gly
 2360 2365 2370

Ala Ala Gly Gly Ala Cys Cys Cys Cys Cys Ala Ala Gly Ala Gly
 2375 2380 2385

Ala Cys Gly Gly Cys Cys Ala Ala Gly Cys Thr Cys Thr Thr Thr
 2390 2395 2400

Thr Cys Ala Gly Thr Gly Cys Cys Ala Gly Ala Cys Thr Thr Thr
 2405 2410 2415

Gly Thr Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Thr Gly Cys
 2420 2425 2430

Ala Ala Ala Gly Cys Cys Ala Thr Cys Gly Cys Ala Thr Cys Cys
 2435 2440 2445

Cys Gly Gly Gly Thr Gly Cys Gly Gly Gly Gly Gly Gly Cys Cys
 2450 2455 2460

Gly Thr Gly Gly Cys Cys Thr Cys Thr Gly Thr Cys Ala Cys Thr
 2465 2470 2475

Thr Thr Cys Gly Ala Thr Gly Ala Cys Thr Thr Cys Cys Ala Thr
 2480 2485 2490

Ala Ala Gly Ala Ala Cys Thr Cys Ala Gly Cys Cys Cys Gly Cys
 2495 2500 2505

Ala Thr Cys Ala Thr Thr Cys Gly Cys Ala Cys Thr Gly Cys Thr

2510	2515	2520
Gly Thr Cys Thr Thr Thr Gly 2525	Gly Gly Cys Thr Thr Thr 2530	Gly Ala Gly 2535
Ala Cys Cys Thr Cys Gly Gly 2540	Ala Ala Gly Cys Gly 2545	Ala Ala Gly 2550
Gly Gly Cys Cys Cys Cys Gly 2555	Ala Thr Gly Gly Cys 2560	Ala Thr Gly 2565
Gly Cys Cys Cys Thr Gly Cys 2570	Cys Cys Ala Gly Gly 2575	Cys Cys Cys 2580
Cys Gly Gly Gly Ala Cys Cys 2585	Ala Gly Gly Cys Thr 2590	Gly Thr Cys 2595
Thr Thr Cys Cys Cys Cys Cys 2600	Ala Ala Ala Ala Cys 2605	Gly Gly Gly 2610
Cys Thr Gly Gly Thr Gly Gly 2615	Thr Cys Ala Gly Cys 2620	Ala Gly Thr 2625
Gly Thr Gly Gly Ala Cys Gly 2630	Thr Gly Cys Ala Gly 2635	Thr Cys Ala 2640
Gly Thr Gly Gly Ala Gly Cys 2645	Cys Thr Gly Thr Gly 2650	Gly Ala Thr 2655
Cys Ala Gly Ala Gly Gly Ala 2660	Cys Cys Cys Gly Gly 2665	Gly Ala Cys 2670
Gly Cys Cys Cys Thr Gly Cys 2675	Ala Ala Cys Gly Cys 2680	Ala Gly Cys 2685
Gly Thr Cys Cys Ala Gly Cys 2690	Thr Gly Gly Cys Cys 2695	Ala Thr Cys 2700
Gly Ala Gly Ala Thr Cys Ala 2705	Cys Cys Ala Cys Cys 2710	Ala Ala Cys 2715
Thr Cys Cys Cys Ala Gly Gly 2720	Ala Ala Gly Cys Gly 2725	Gly Cys Gly 2730

Gly Cys Cys Ala Ala Gly Cys Ala Thr Gly Ala Gly Gly Cys Thr
 2735 2740 2745

Cys Ala Gly Ala Gly Ala Cys Thr Gly Gly Ala Gly Cys Ala Gly
 2750 2755 2760

Gly Ala Ala Gly Cys Cys Cys Gly Cys Gly Gly Cys Cys Gly Gly
 2765 2770 2775

Cys Thr Thr Gly Ala Gly Cys Gly Gly Cys Ala Gly Ala Ala Gly
 2780 2785 2790

Ala Thr Cys Cys Thr Gly Gly Ala Cys Cys Ala Gly Thr Cys Ala
 2795 2800 2805

Gly Ala Ala Gly Cys Cys Gly Ala Gly Ala Ala Ala Gly Cys Thr
 2810 2815 2820

Cys Gly Cys Ala Ala Gly Gly Ala Ala Cys Thr Thr Thr Thr Gly
 2825 2830 2835

Gly Ala Gly Cys Thr Gly Gly Ala Gly Gly Cys Thr Cys Thr Gly
 2840 2845 2850

Ala Gly Cys Ala Thr Gly Gly Cys Cys Gly Thr Gly Gly Ala Gly
 2855 2860 2865

Ala Gly Cys Ala Cys Cys Gly Gly Gly Ala Cys Thr Gly Cys Cys
 2870 2875 2880

Ala Ala Gly Gly Cys Gly Gly Ala Gly Gly Cys Cys Gly Ala Gly
 2885 2890 2895

Thr Cys Cys Cys Gly Thr Gly Cys Gly Gly Ala Gly Gly Cys Ala
 2900 2905 2910

Gly Cys Cys Cys Gly Gly Ala Thr Thr Gly Ala Gly Gly Gly Ala
 2915 2920 2925

Gly Ala Ala Gly Gly Gly Thr Cys Cys Gly Thr Gly Cys Thr Gly
 2930 2935 2940

Cys Ala Gly Gly Cys Cys Ala Ala Gly Cys Thr Ala Ala Ala Ala
 2945 2950 2955

Gly Cys 2960	Ala Cys Ala Gly Gly 2965	Cys Cys Thr Thr Gly 2970	Gly Cys Cys
Ala Thr 2975	Thr Gly Ala Ala Ala 2980	Cys Gly Gly Ala Gly 2985	Gly Cys Thr
Gly Ala 2990	Gly Cys Thr Cys Cys 2995	Ala Gly Ala Gly Gly 3000	Gly Thr Cys
Cys Ala 3005	Gly Ala Ala Gly Gly 3010	Thr Cys Cys Gly Ala 3015	Gly Ala Gly
Cys Thr 3020	Gly Gly Ala Ala Cys 3025	Thr Gly Gly Thr Cys 3030	Thr Ala Thr
Gly Cys 3035	Cys Cys Gly Gly Gly 3040	Cys Cys Cys Ala Gly 3045	Cys Thr Gly
Gly Ala 3050	Gly Cys Thr Gly Gly 3055	Ala Gly Gly Thr Gly 3060	Ala Gly Cys
Ala Ala 3065	Gly Gly Cys Thr Cys 3070	Ala Gly Cys Ala Gly 3075	Cys Thr Gly
Gly Cys 3080	Thr Gly Ala Gly Gly 3085	Thr Gly Gly Ala Gly 3090	Gly Thr Gly
Ala Ala 3095	Gly Ala Ala Gly Thr 3100	Thr Cys Ala Ala Gly 3105	Cys Ala Gly
Ala Thr 3110	Gly Ala Cys Ala Gly 3115	Ala Gly Gly Cys Cys 3120	Ala Thr Ala
Gly Gly 3125	Cys Cys Cys Cys Ala 3130	Gly Cys Ala Cys Cys 3135	Ala Thr Cys
Ala Gly 3140	Gly Gly Ala Cys Cys 3145	Thr Thr Gly Cys Thr 3150	Gly Thr Gly
Gly Cys 3155	Thr Gly Gly Gly Cys 3160	Cys Thr Gly Ala Gly 3165	Ala Thr Gly
Cys Ala	Gly Gly Thr Ala Ala	Ala Ala Cys Thr Gly	Cys Thr Cys

3170	3175	3180
Cys Ala Gly Thr Cys Cys Cys Thr Gly Gly Gly Cys Cys Thr Gly		
3185	3190	3195
Ala Ala Ala Thr Cys Ala Ala Cys Cys Cys Thr Cys Ala Thr Cys		
3200	3205	3210
Ala Cys Cys Gly Ala Thr Gly Gly Cys Thr Cys Cys Ala Cys Thr		
3215	3220	3225
Cys Cys Cys Ala Thr Cys Ala Ala Cys Cys Thr Cys Thr Thr Cys		
3230	3235	3240
Ala Ala Cys Ala Cys Ala Gly Cys Cys Thr Thr Thr Gly Gly Gly		
3245	3250	3255
Cys Thr Gly Cys Thr Gly Gly Gly Gly Ala Thr Gly Gly Gly Gly		
3260	3265	3270
Cys Cys Cys Gly Ala Gly Gly Gly Thr Cys Ala Gly Cys Cys Cys		
3275	3280	3285
Cys Thr Gly Gly Gly Cys Ala Gly Ala Ala Gly Gly Gly Thr Gly		
3290	3295	3300
Gly Cys Cys Ala Gly Thr Gly Gly Gly Cys Cys Cys Ala Gly Cys		
3305	3310	3315
Cys Cys Thr Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala Thr Ala		
3320	3325	3330
Thr Cys Cys Cys Cys Cys Cys Ala Gly Thr Cys Thr Gly Cys Thr		
3335	3340	3345
Cys Ala Gly Gly Cys Cys Cys Cys Thr Cys Ala Ala Gly Cys Thr		
3350	3355	3360
Cys Cys Thr Gly Gly Ala Gly Ala Cys Ala Ala Cys Cys Ala Cys		
3365	3370	3375
Gly Thr Gly Gly Thr Gly Cys Cys Thr Gly Thr Ala Cys Thr Gly		
3380	3385	3390

Cys Gly Cys Thr Ala Ala
3395

<210> 48
<211> 1100
<212> PRT
<213> Artificial Sequence

<220>
<223> synthesized and Rattus norvegicus

<400> 48

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Met
 225 230 235 240

Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His
 245 250 255

Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys
 260 265 270

Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg
 275 280 285

Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val
 290 295 300

Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val
 305 310 315 320

Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe
 325 330 335

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln
 340 345 350

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe
 355 360 365

Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe
 370 375 380

Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu
 385 390 395 400

Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg
 405 410 415

Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr Gly
 420 425 430

Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val Phe
 435 440 445

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr
 450 455 460

Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly Val
 465 470 475 480

Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu
 485 490 495

Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro Ile
 500 505 510

Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met Gly
 515 520 525

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu
 530 535 540

Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile Gln
 545 550 555 560

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala Leu
 565 570 575

Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln Ala
 580 585 590

Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala
 595 600 605

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln Asn
 610 615 620

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val
 625 630 635 640

Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys

645	650	655
Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro		
660	665	670
Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser		
675	680	685
Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn		
690	695	700
Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val		
705	710	715
Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val		
725	730	735
Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala		
740	745	750
Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile		
755	760	765
Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp		
770	775	780
His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys Leu		
785	790	795
Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser		
805	810	815
Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys		
820	825	830
Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met Ser		
835	840	845
Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp Gln		
850	855	860
Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln		
865	870	875
		880

146/429

<210> 49
 <211> 3303
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 49

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Ala Ala Cys Thr Gly Thr Thr Cys Ala Cys Thr Gly Gly Cys Gly Thr
 20 25 30

Gly Gly Thr Cys Cys Cys Ala Ala Thr Thr Cys Thr Cys Gly Thr Gly
 35 40 45

Gly Ala Ala Cys Thr Gly Gly Ala Thr Gly Gly Cys Gly Ala Thr Gly
 50 55 60

Thr Gly Ala Ala Thr Gly Gly Gly Cys Ala Cys Ala Ala Ala Thr Thr
 65 70 75 80

Thr Thr Cys Thr Gly Thr Cys Ala Gly Cys Gly Gly Ala Gly Ala Gly
 85 90 95

Gly Gly Thr Gly Ala Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Ala
 100 105 110

Cys Ala Thr Ala Cys Gly Gly Ala Ala Ala Gly Cys Thr Cys Ala Cys
 115 120 125

Cys Cys Thr Gly Ala Ala Ala Thr Thr Cys Ala Thr Cys Thr Gly Cys
 130 135 140

Ala Cys Cys Ala Cys Thr Gly Gly Ala Ala Ala Gly Cys Thr Cys Cys
 145 150 155 160

Cys Thr Gly Thr Gly Cys Cys Ala Thr Gly Gly Cys Cys Ala Ala Cys
 165 170 175

Ala Cys Thr Gly Gly Thr Cys Ala Cys Thr Ala Cys Cys Thr Thr Cys
 180 185 190

Ala Cys Cys Thr Ala Thr Gly Gly Cys Gly Thr Gly Cys Ala Gly Thr
 195 200 205

Gly Cys Thr Thr Thr Thr Cys Cys Ala Gly Ala Thr Ala Cys Cys Cys
 210 215 220

Ala Gly Ala Cys Cys Ala Thr Ala Thr Gly Ala Ala Gly Cys Ala Gly
 225 230 235 240

Cys Ala Thr Gly Ala Cys Thr Thr Thr Thr Thr Cys Ala Ala Gly Ala
 245 250 255

Gly Cys Gly Cys Cys Ala Thr Gly Cys Cys Cys Gly Ala Gly Gly Gly
 260 265 270

Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Gly Ala Gly Ala
 275 280 285

Ala Cys Cys Ala Thr Cys Thr Thr Thr Thr Thr Cys Ala Ala Ala Gly
 290 295 300

Ala Thr Gly Ala Cys Gly Gly Gly Ala Ala Cys Thr Ala Cys Ala Ala
 305 310 315 320

Gly Ala Cys Cys Cys Gly Cys Gly Cys Thr Gly Ala Ala Gly Thr Cys
 325 330 335

Ala Ala Gly Thr Thr Cys Gly Ala Ala Gly Gly Thr Gly Ala Cys Ala
 340 345 350

Cys Cys Cys Thr Gly Gly Thr Gly Ala Ala Thr Ala Gly Ala Ala Thr
 355 360 365

Cys Gly Ala Gly Cys Thr Gly Ala Ala Gly Gly Gly Cys Ala Thr Thr
 370 375 380

Gly Ala Cys Thr Thr Thr Ala Ala Gly Gly Ala Gly Gly Ala Thr Gly
 385 390 395 400

Gly Ala Ala Ala Cys Ala Thr Thr Cys Thr Cys Gly Gly Cys Cys Ala
 405 410 415

Cys Ala Ala Gly Cys Thr Gly Gly Ala Ala Thr Ala Cys Ala Ala Cys
 420 425 430

Thr Ala Thr Ala Ala Cys Thr Cys Cys Cys Ala Cys Ala Ala Thr Gly
 435 440 445

Thr Gly Thr Ala Cys Ala Thr Cys Ala Thr Gly Gly Cys Cys Gly Ala
 450 455 460

Cys Ala Ala Gly Cys Ala Ala Ala Ala Gly Ala Ala Thr Gly Gly Cys
 465 470 475 480

Ala Thr Cys Ala Ala Gly Gly Thr Cys Ala Ala Cys Thr Thr Cys Ala
 485 490 495

Ala Gly Ala Thr Cys Ala Gly Ala Cys Ala Cys Ala Ala Cys Ala Thr
 500 505 510

Thr Gly Ala Gly Gly Ala Thr Gly Gly Ala Thr Cys Cys Gly Thr Gly
 515 520 525

Cys Ala Gly Cys Thr Gly Gly Cys Cys Gly Ala Cys Cys Ala Thr Thr
 530 535 540

Ala Thr Cys Ala Ala Cys Ala Gly Ala Ala Cys Ala Cys Thr Cys Cys
 545 550 555 560

Ala Ala Thr Cys Gly Gly Cys Gly Ala Cys Gly Gly Cys Cys Cys Thr
 565 570 575

Gly Thr Gly Cys Thr Cys Cys Thr Cys Cys Cys Ala Gly Ala Cys Ala
 580 585 590

Ala Cys Cys Ala Thr Thr Ala Cys Cys Thr Gly Thr Cys Cys Ala Cys
 595 600 605

Cys Cys Ala Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Thr Cys Thr
 610 615 620

Ala Ala Ala Gly Ala Thr Cys Cys Cys Ala Ala Cys Gly Ala Ala Ala
 625 630 635 640

Ala Gly Ala Gly Ala Gly Ala Cys Cys Ala Cys Ala Thr Gly Gly Thr
 645 650 655

Cys Cys Thr Gly Cys Thr Gly Gly Ala Gly Thr Thr Thr Gly Thr Gly

660	665	670
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Cys Ala Cys Ala Thr Gly Gly Cys Ala Thr Gly Gly Ala Cys Gly Ala 690 695 700		
Gly Cys Thr Gly Thr Ala Cys Ala Ala Gly Cys Cys Cys Ala Thr Gly 705 710 715 720		
Gly Cys Ala Ala Cys Thr Gly Ala Ala Gly Ala Gly Gly Cys Cys Ala 725 730 735		
Thr Cys Ala Thr Cys Cys Gly Cys Ala Thr Cys Cys Cys Cys Cys Cys 740 745 750		
Ala Thr Ala Cys Cys Ala Cys Thr Ala Cys Ala Thr Cys Cys Ala Thr 755 760 765		
Gly Thr Gly Cys Thr Gly Gly Ala Cys Cys Ala Gly Ala Ala Cys Ala 770 775 780		
Gly Thr Ala Ala Thr Gly Thr Gly Thr Cys Cys Cys Gly Thr Gly Thr 785 790 795 800		
Gly Gly Ala Gly Gly Thr Thr Gly Gly Ala Cys Cys Ala Ala Ala Gly 805 810 815		
Ala Cys Cys Thr Ala Cys Ala Thr Cys Cys Gly Gly Cys Ala Gly Gly 820 825 830		
Ala Cys Ala Ala Thr Gly Ala Gly Ala Gly Gly Gly Thr Ala Cys Thr 835 840 845		
Gly Thr Thr Thr Gly Cys Cys Cys Cys Ala Gly Thr Thr Cys Gly Cys 850 855 860		
Ala Thr Gly Gly Thr Gly Ala Cys Cys Gly Thr Cys Cys Cys Cys Cys 865 870 875 880		
Cys Ala Cys Gly Cys Cys Ala Cys Thr Ala Cys Thr Gly Cys Ala Thr 885 890 895		

Ala Gly Thr Gly Gly Cys Cys Ala Ala Cys Cys Cys Thr Gly Thr Gly
 900 905 910

Thr Cys Cys Cys Gly Gly Gly Ala Cys Ala Cys Cys Cys Ala Gly Ala
 915 920 925

Gly Thr Thr Cys Thr Gly Thr Gly Thr Thr Ala Thr Thr Thr Gly Ala
 930 935 940

Cys Ala Thr Cys Ala Cys Ala Gly Gly Ala Cys Ala Ala Gly Thr Cys
 945 950 955 960

Cys Gly Ala Cys Thr Cys Cys Gly Gly Cys Ala Cys Gly Cys Thr Gly
 965 970 975

Ala Cys Cys Ala Gly Gly Ala Gly Ala Thr Cys Cys Gly Ala Cys Thr
 980 985 990

Ala Gly Cys Cys Cys Ala Gly Gly Ala Cys Cys Cys Cys Thr Thr Cys
 995 1000 1005

Cys Cys Cys Cys Thr Gly Thr Ala Thr Cys Cys Ala Gly Gly Gly
 1010 1015 1020

Gly Ala Gly Gly Thr Gly Cys Thr Gly Gly Ala Ala Ala Ala Gly
 1025 1030 1035

Gly Ala Cys Ala Thr Cys Ala Cys Cys Cys Cys Ala Cys Thr Gly
 1040 1045 1050

Cys Ala Gly Gly Thr Gly Gly Thr Thr Cys Thr Gly Cys Cys Cys
 1055 1060 1065

Ala Ala Cys Ala Cys Ala Gly Cys Ala Cys Thr Gly Cys Ala Thr
 1070 1075 1080

Cys Thr Thr Ala Ala Gly Gly Cys Gly Thr Thr Gly Cys Thr Gly
 1085 1090 1095

Gly Ala Cys Thr Thr Thr Gly Ala Gly Gly Ala Thr Ala Ala Gly
 1100 1105 1110

Ala Ala Thr Gly Gly Ala Gly Ala Cys Ala Ala Gly Gly Thr Cys
 1115 1120 1125

Ala Thr Gly Gly Cys Ala Gly Gly Ala Gly Ala Cys Gly Ala Gly
1130 1135 1140

Thr Gly Gly Cys Thr Ala Thr Thr Thr Gly Ala Gly Gly Gly Ala
1145 1150 1155

Cys Cys Thr Gly Gly Cys Ala Cys Cys Thr Ala Cys Ala Thr Cys
1160 1165 1170

Cys Cys Ala Cys Ala Gly Ala Ala Gly Gly Ala Ala Gly Thr Gly
1175 1180 1185

Gly Ala Ala Gly Thr Cys Gly Thr Gly Gly Ala Gly Ala Thr Cys
1190 1195 1200

Ala Thr Thr Cys Ala Gly Gly Cys Cys Ala Cys Ala Gly Thr Cys
1205 1210 1215

Ala Thr Cys Ala Ala Ala Cys Ala Gly Ala Ala Cys Cys Ala Ala
1220 1225 1230

Gly Cys Ala Cys Thr Gly Cys Gly Gly Cys Thr Ala Ala Gly Gly
1235 1240 1245

Gly Cys Cys Cys Gly Ala Ala Ala Gly Gly Ala Gly Thr Gly Cys
1250 1255 1260

Thr Thr Thr Gly Ala Cys Cys Gly Gly Gly Ala Gly Gly Gly Cys
1265 1270 1275

Ala Ala Gly Gly Gly Gly Cys Gly Cys Gly Thr Gly Ala Cys Ala
1280 1285 1290

Gly Gly Thr Gly Ala Gly Gly Ala Gly Thr Gly Gly Cys Thr Gly
1295 1300 1305

Gly Thr Cys Cys Gly Ala Thr Cys Cys Gly Thr Gly Gly Gly Gly
1310 1315 1320

Gly Cys Thr Thr Ala Cys Cys Thr Cys Cys Cys Ala Gly Cys Thr
1325 1330 1335

Gly Thr Cys Thr Thr Thr Gly Ala Ala Gly Ala Gly Gly Thr Gly

1340		1345		1350
Cys Thr Gly Gly Ala Thr	Cys Thr Gly Gly Thr	Gly Gly Ala Thr		
1355	1360	1365		
Gly Cys Thr Gly Thr Gly	Ala Thr Cys Cys Thr	Thr Ala Cys Ala		
1370	1375	1380		
Gly Ala Ala Ala Ala Gly	Ala Cys Thr Gly Cys	Cys Cys Thr Gly		
1385	1390	1395		
Cys Ala Cys Cys Thr Cys	Cys Gly Gly Gly Cys	Thr Cys Thr Gly		
1400	1405	1410		
Cys Ala Gly Ala Ala Cys	Thr Thr Cys Ala Gly	Gly Gly Ala Cys		
1415	1420	1425		
Cys Thr Thr Cys Gly Gly	Gly Gly Ala Gly Thr	Gly Cys Thr Cys		
1430	1435	1440		
Cys Ala Cys Cys Gly Cys	Ala Cys Cys Gly Gly	Gly Gly Ala Gly		
1445	1450	1455		
Gly Ala Ala Thr Gly Gly	Thr Thr Ala Gly Thr	Gly Ala Cys Ala		
1460	1465	1470		
Gly Thr Gly Cys Ala Gly	Gly Ala Cys Ala Cys	Ala Gly Ala Ala		
1475	1480	1485		
Gly Cys Cys Cys Ala Thr	Gly Thr Thr Cys Cys	Ala Gly Ala Thr		
1490	1495	1500		
Gly Thr Cys Thr Ala Thr	Gly Ala Gly Gly Ala	Gly Gly Thr Gly		
1505	1510	1515		
Cys Thr Thr Gly Gly Gly	Gly Thr Ala Gly Thr	Ala Cys Cys Cys		
1520	1525	1530		
Ala Thr Cys Ala Cys Cys	Ala Cys Cys Cys Thr	Gly Gly Gly Ala		
1535	1540	1545		
Cys Cys Thr Cys Gly Ala	Cys Ala Cys Thr Ala	Cys Thr Gly Thr		
1550	1555	1560		

Gly Thr Cys Ala Thr Thr Cys Thr Thr Gly Ala Cys Cys Cys Ala
 1565 1570 1575

Ala Thr Gly Gly Gly Ala Cys Cys Ala Gly Ala Cys Gly Gly Cys
 1580 1585 1590

Ala Ala Gly Ala Ala Cys Cys Ala Gly Cys Thr Gly Gly Gly Ala
 1595 1600 1605

Cys Ala Ala Ala Ala Gly Cys Gly Thr Gly Thr Thr Gly Thr Cys
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Ala Ala Gly Gly Gly Ala Gly Ala Gly Ala Ala Gly Thr Cys Cys
 1625 1630 1635

Thr Thr Thr Thr Thr Cys Cys Thr Cys Cys Ala Gly Cys Cys Ala
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Gly Gly Ala Gly Ala Gly Ala Gly Gly Cys Thr Gly Gly Ala Gly
 1655 1660 1665

Cys Gly Ala Gly Gly Cys Ala Thr Cys Cys Ala Gly Gly Ala Thr
 1670 1675 1680

Gly Thr Gly Thr Ala Thr Gly Thr Gly Cys Thr Gly Thr Cys Ala
 1685 1690 1695

Gly Ala Gly Cys Ala Gly Cys Ala Gly Gly Gly Gly Cys Thr Gly
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Cys Thr Ala Cys Thr Gly Ala Ala Gly Gly Cys Ala Cys Thr Gly
 1715 1720 1725

Cys Ala Gly Cys Cys Cys Cys Thr Gly Gly Ala Gly Gly Ala Gly
 1730 1735 1740

Gly Gly Ala Gly Ala Gly Ala Gly Cys Gly Ala Gly Gly Ala Gly
 1745 1750 1755

Ala Ala Gly Gly Thr Cys Thr Cys Cys Cys Ala Thr Cys Ala Gly
 1760 1765 1770

Gly Cys Cys Gly Gly Ala Gly Ala Cys Thr Gly Cys Thr Gly Gly
 1775 1780 1785

Cys Thr Cys Ala Thr Cys Cys Gly Thr Gly Gly Gly Cys Cys Cys
 1790 1795 1800

Cys Thr Gly Gly Ala Gly Thr Ala Thr Gly Thr Gly Cys Cys Ala
 1805 1810 1815

Thr Cys Thr Gly Cys Ala Ala Ala Ala Gly Thr Gly Gly Ala Gly
 1820 1825 1830

Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Gly Thr
 1835 1840 1845

Cys Ala Gly Gly Cys Thr Ala Thr Cys Cys Cys Thr Cys Thr Gly
 1850 1855 1860

Gly Ala Cys Cys Ala Ala Ala Ala Thr Gly Ala Gly Gly Gly Cys
 1865 1870 1875

Ala Thr Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Thr
 1880 1885 1890

Gly Thr Cys Ala Ala Gly Ala Cys Gly Gly Gly Gly Ala Ala Gly
 1895 1900 1905

Gly Thr Gly Cys Gly Gly Gly Cys Thr Gly Thr Gly Ala Thr Thr
 1910 1915 1920

Gly Gly Ala Ala Gly Cys Ala Cys Cys Thr Ala Cys Ala Thr Gly
 1925 1930 1935

Cys Thr Gly Ala Cys Thr Cys Ala Gly Gly Ala Thr Gly Ala Ala
 1940 1945 1950

Gly Thr Cys Cys Thr Gly Thr Gly Gly Gly Ala Ala Ala Ala Gly
 1955 1960 1965

Gly Ala Gly Cys Thr Gly Cys Cys Thr Thr Cys Thr Gly Gly Gly
 1970 1975 1980

Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Thr Gly Cys Thr Gly
 1985 1990 1995

Ala Ala Cys Thr Thr Gly Gly Gly Gly Cys Ala Thr Gly Ala Cys

2000	2005	2010
Cys Cys Thr Cys Thr Gly Gly 2015	Cys Ala Gly Ala Cys 2020	Cys Ala Gly Gly 2025
Gly Gly Thr Cys Ala Gly Ala 2030	Ala Gly Gly Gly Cys 2035	Ala Cys Ala 2040
Gly Cys Cys Ala Ala Gly Cys 2045	Cys Cys Cys Thr Thr 2050	Cys Ala Gly 2055
Cys Cys Cys Thr Cys Ala Gly 2060	Cys Thr Cys Cys Ala 2065	Ala Gly Gly 2070
Ala Ala Cys Ala Ala Gly Ala 2075	Cys Cys Cys Gly Ala 2080	Gly Thr Gly 2085
Gly Thr Cys Ala Gly Cys Thr 2090	Ala Cys Cys Gly Thr 2095	Gly Thr Cys 2100
Cys Cys Gly Cys Ala Cys Ala 2105	Ala Thr Gly Cys Ala 2110	Gly Cys Gly 2115
Gly Thr Gly Cys Ala Gly Gly 2120	Thr Cys Thr Ala Thr 2125	Gly Ala Cys 2130
Thr Ala Cys Ala Gly Ala Gly 2135	Cys Cys Ala Ala Gly 2140	Ala Gly Ala 2145
Gly Cys Cys Cys Gly Thr Gly 2150	Thr Gly Gly Thr Cys 2155	Thr Thr Thr 2160
Gly Gly Gly Cys Cys Cys Gly 2165	Ala Gly Cys Thr Ala 2170	Gly Thr Gly 2175
Ala Cys Ala Cys Thr Gly Gly 2180	Ala Thr Cys Cys Thr 2185	Gly Ala Gly 2190
Gly Ala Gly Cys Ala Gly Thr 2195	Thr Cys Ala Cys Ala 2200	Gly Thr Ala 2205
Thr Thr Gly Thr Cys Cys Cys 2210	Thr Thr Thr Cys Thr 2215	Gly Cys Cys 2220

Gly Gly Gly Cys Gly Ala Cys Cys Cys Ala Ala Gly Cys Gly Thr
 2225 2230 2235

Cys Cys Thr Cys Ala Thr Gly Cys Cys Cys Gly Cys Cys Gly Thr
 2240 2245 2250

Gly Cys Ala Cys Thr Cys Thr Gly Cys Cys Thr Ala Cys Thr Gly
 2255 2260 2265

Cys Thr Gly Gly Gly Ala Cys Cys Thr Gly Ala Thr Thr Thr Cys
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Thr Thr Thr Ala Cys Thr Gly Ala Thr Gly Thr Cys Ala Thr Cys
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 2390 2395 2400

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Gly Thr Gly Gly Gly Thr Gly Ala Cys Gly Cys Cys Thr Gly Cys
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Ala Ala Gly Gly Cys Cys Ala Thr Thr Gly Cys Ala Thr Cys Cys
 2435 2440 2445

Cys Gly Ala Gly Thr Cys Cys Gly Gly Gly Gly Gly Gly Cys Thr
 2450 2455 2460
 Gly Thr Ala Gly Cys Cys Thr Cys Thr Gly Thr Cys Ala Cys Cys
 2465 2470 2475
 Thr Thr Thr Gly Ala Thr Gly Ala Cys Thr Thr Cys Cys Ala Thr
 2480 2485 2490
 Ala Ala Ala Ala Ala Cys Thr Cys Ala Gly Cys Cys Cys Gly Gly
 2495 2500 2505
 Ala Thr Cys Ala Thr Thr Cys Gly Ala Ala Thr Gly Gly Cys Thr
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 Gly Thr Thr Thr Thr Thr Gly Gly Cys Thr Thr Thr Gly Ala Gly
 2525 2530 2535
 Ala Thr Gly Thr Cys Thr Gly Ala Ala Gly Ala Cys Ala Cys Ala
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 Gly Gly Thr Cys Cys Thr Gly Ala Thr Gly Gly Cys Ala Cys Ala
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 Cys Thr Cys Cys Thr Gly Cys Cys Cys Ala Ala Gly Gly Cys Thr
 2570 2575 2580
 Cys Gly Ala Gly Ala Cys Cys Ala Gly Gly Cys Ala Gly Thr Cys
 2585 2590 2595
 Thr Thr Thr Cys Cys Cys Cys Ala Ala Ala Ala Cys Gly Gly Gly
 2600 2605 2610
 Cys Thr Gly Gly Thr Ala Gly Thr Cys Ala Gly Cys Ala Gly Thr
 2615 2620 2625
 Gly Thr Gly Gly Ala Thr Gly Thr Gly Cys Ala Gly Thr Cys Ala
 2630 2635 2640
 Gly Thr Gly Gly Ala Gly Cys Cys Cys Gly Thr Gly Gly Ala Cys
 2645 2650 2655
 Cys Ala Gly Ala Gly Gly Ala Cys Cys Cys Gly Gly Gly Ala Thr

2660		2665		2670
Gly Cys Cys Cys Thr Thr Cys Ala Gly Cys Gly Cys Ala Gly Cys				
2675		2680		2685
Gly Thr Thr Cys Ala Gly Cys Thr Gly Gly Cys Cys Ala Thr Cys				
2690		2695		2700
Gly Ala Ala Ala Thr Thr Ala Cys Cys Ala Cys Cys Ala Ala Cys				
2705		2710		2715
Thr Cys Cys Cys Ala Gly Gly Ala Gly Gly Cys Ala Gly Cys Ala				
2720		2725		2730
Gly Cys Cys Ala Ala Gly Cys Ala Cys Gly Ala Gly Gly Cys Thr				
2735		2740		2745
Cys Ala Gly Ala Gly Ala Cys Thr Gly Gly Ala Ala Cys Ala Gly				
2750		2755		2760
Gly Ala Ala Gly Cys Cys Cys Gly Thr Gly Gly Thr Cys Gly Gly				
2765		2770		2775
Cys Thr Thr Gly Ala Gly Ala Gly Gly Cys Ala Gly Ala Ala Gly				
2780		2785		2790
Ala Thr Cys Thr Thr Gly Gly Ala Cys Cys Ala Gly Thr Cys Ala				
2795		2800		2805
Gly Ala Ala Gly Cys Thr Gly Ala Ala Ala Ala Ala Gly Cys Cys				
2810		2815		2820
Cys Gly Cys Ala Ala Gly Gly Ala Ala Cys Thr Cys Thr Thr Gly				
2825		2830		2835
Gly Ala Gly Cys Thr Thr Gly Ala Gly Gly Cys Thr Ala Thr Gly				
2840		2845		2850
Ala Gly Cys Ala Thr Gly Gly Cys Thr Gly Thr Gly Gly Ala Gly				
2855		2860		2865
Ala Gly Cys Ala Cys Gly Gly Gly Thr Ala Ala Thr Gly Cys Cys				
2870		2875		2880

Ala Ala Ala Gly Cys Ala Gly Ala Gly Gly Cys Thr Gly Ala Gly
 2885 2890 2895

Thr Cys Cys Cys Gly Thr Gly Cys Ala Gly Ala Gly Gly Cys Ala
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Gly Cys Gly Ala Gly Gly Ala Thr Cys Gly Ala Ala Gly Gly Ala
 2915 2920 2925

Gly Ala Ala Gly Gly Cys Thr Cys Thr Gly Thr Gly Cys Thr Gly
 2930 2935 2940

Cys Ala Gly Gly Cys Cys Ala Ala Gly Cys Thr Cys Ala Ala Gly
 2945 2950 2955

Gly Cys Ala Cys Ala Gly Gly Cys Gly Cys Thr Ala Gly Cys Cys
 2960 2965 2970

Ala Thr Thr Gly Ala Gly Ala Cys Gly Gly Ala Gly Gly Cys Thr
 2975 2980 2985

Gly Ala Gly Thr Thr Gly Gly Ala Gly Cys Gly Ala Gly Thr Ala
 2990 2995 3000

Ala Ala Gly Ala Ala Ala Gly Thr Ala Cys Gly Ala Gly Ala Gly
 3005 3010 3015

Ala Thr Gly Gly Ala Ala Cys Thr Gly Ala Thr Cys Thr Ala Thr
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Gly Cys Cys Cys Gly Gly Gly Cys Cys Cys Ala Gly Thr Thr Gly
 3035 3040 3045

Gly Ala Gly Cys Thr Gly Gly Ala Gly Gly Thr Gly Ala Gly Cys
 3050 3055 3060

Ala Ala Gly Gly Cys Gly Cys Ala Gly Cys Ala Gly Cys Thr Thr
 3065 3070 3075

Gly Cys Cys Ala Ala Thr Gly Thr Gly Gly Ala Gly Gly Cys Ala
 3080 3085 3090

Ala Ala Gly Ala Ala Gly Thr Thr Cys Ala Ala Gly Gly Ala Gly
 3095 3100 3105

Ala Thr Gly Ala Cys Ala Gly Ala Gly Gly Cys Ala Cys Thr Gly
 3110 3115 3120

Gly Gly Cys Cys Cys Cys Gly Gly Cys Ala Cys Cys Ala Thr Cys
 3125 3130 3135

Ala Gly Gly Gly Ala Cys Cys Thr Gly Gly Cys Thr Gly Thr Gly
 3140 3145 3150

Gly Cys Cys Gly Gly Gly Cys Cys Ala Gly Ala Gly Ala Thr Gly
 3155 3160 3165

Cys Ala Gly Gly Thr Gly Ala Ala Ala Cys Thr Thr Cys Thr Cys
 3170 3175 3180

Cys Ala Gly Thr Cys Cys Cys Thr Gly Gly Gly Cys Cys Thr Gly
 3185 3190 3195

Ala Ala Ala Thr Cys Cys Ala Cys Thr Cys Thr Cys Ala Thr Cys
 3200 3205 3210

Ala Cys Cys Gly Ala Thr Gly Gly Cys Thr Cys Gly Thr Cys Thr
 3215 3220 3225

Cys Cys Cys Ala Thr Cys Ala Ala Cys Cys Thr Cys Thr Thr Cys
 3230 3235 3240

Ala Gly Cys Ala Cys Ala Gly Cys Cys Thr Thr Cys Gly Gly Gly
 3245 3250 3255

Thr Thr Gly Cys Thr Gly Gly Gly Gly Cys Thr Gly Gly Gly Gly
 3260 3265 3270

Thr Cys Thr Gly Ala Thr Gly Gly Thr Cys Ala Gly Cys Cys Gly
 3275 3280 3285

Cys Cys Ala Gly Cys Ala Cys Ala Gly Ala Ala Gly Thr Gly Ala
 3290 3295 3300

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 <211> 267
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 50

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Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser
 20 25 30

Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val
 35 40 45

Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser
 50 55 60

Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys Phe
 65 70 75 80

Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu
 85 90 95

Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln Asp
 100 105 110

Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe
 115 120 125

Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn
 130 135 140

Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln Ser Leu Gly Val
 145 150 155 160

Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val Leu
 165 170 175

Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe Lys Ser
 180 185 190

Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala
 195 200 205

Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg Arg Thr Glu Gly

210	215	220
Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp		
225	230	235 240
Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser		
245	250	255
Pro Leu His Arg Val Leu His Tyr Ser Gln Gly		
260	265	

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 <212> DNA
 <213> Artificial Sequence

<220>
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 ctctgtcttc tagaagaatc agtaggcagt ctgaaggaa gtcgatgtcc tgtctttgct 180
 tttcaaagtt ctgacacaga aagtgatgag ctatcagaag tacttcaaga cagctgcttt 240
 ttacaaataa agtgtgatac aaaagatgac agtatcccggt gctttctgga attaaaagaa 300
 gaggatgaaa tagtgtgcac acaacactgg caggatgctg tgccttggac agaactcctc 360
 agtctacaga cagaggatgg cttctggaaa ottacaccag aactgggact tatattaaat 420
 cttaatacaa atggtttgca cagctttctt aaacaaaaag gcattcaatc tctaggtgta 480
 aaaggaagag aatgtctcct ggacctaatt gccacaatgc tggactaca gtttattcgc 540
 accagggttg aaaaagaggg aatagtgttc aaatcactga tgaaaatgga tgacccttct 600
 atttccagga atattccctg ggcttttgag gcaataaagc aagcaagtga atgggtaaga 660
 agaactgaag gacagtaccc atctatctgc ccacggcttg aactggggaa cgactgggac 720
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 20 25 30

Gln Gln Lys Lys Lys Leu Gln Thr Asp Ile Lys Glu Asn Gly Gly Lys
 35 40 45

Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile Ile Leu Asp Asn
 50 55 60

Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile Gln Lys Asn His
 65 70 75 80

Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser Ile Arg Glu Lys
 85 90 95

Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys Pro Leu Asp Ile
 100 105 110

Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu Val Lys Thr Glu
 115 120 125

Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp Thr Val Glu Leu
 130 135 140

Thr Glu Phe Gly Met Gln Asn Val Glu Ile Pro His Leu Pro Gln Asp
 145 150 155 160

Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val Gly Met Glu Gly
 165 170 175

Gly Gln Glu Ala Val Val Val Glu Leu Gln Cys Ser Arg Asp Ser Arg
 180 185 190

Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu Asp Asp Gly Met
 195 200 205

Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser Glu Asp Ala Ser

165/429

Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile Leu Cys Arg Gly
 450 455 460

Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val Gln Arg Thr Asp
 465 470 475 480

Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp Ser Leu Ser Thr
 485 490 495

Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly Thr Arg Leu Leu
 500 505 510

Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp Leu His Glu Lys
 515 520 525

Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp Ser Val His Gly
 530 535 540

Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu Asp Asp Glu Phe
 545 550 555 560

Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr Ile Ile Lys Phe
 565 570 575

Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro Ser Asp His Thr
 580 585 590

Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe Ser Lys Val Glu
 595 600 605

Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser Thr Lys Ala Gly
 610 615 620

Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu Asp Val His Ile
 625 630 635 640

Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile Val Phe Gln Thr
 645 650 655

Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys Tyr Ile Phe Pro
 660 665 670

Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala Phe Ile Asn Gly
 675 680 685

Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu Ala Gln Gln Glu
 690 695 700

Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr Leu Met Ser Gln
 705 710 715 720

Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn Leu Pro Pro Lys
 725 730 735

Ala Lys Val Leu Ile Lys Ile Thr Tyr Ile Thr Glu Leu Ser Ile Leu
 740 745 750

Gly Thr Val Gly Val Phe Phe Met Pro Ala Thr Val Ala Pro Trp Gln
 755 760 765

Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln Asp Thr Val Glu Lys Ile
 770 775 780

Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser Leu Thr Met Ser
 785 790 795 800

Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser Asp Thr His Glu
 805 810 815

Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val Ile Ser Thr Met Glu
 820 825 830

Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser Leu His Ile Gly Leu Ser
 835 840 845

Ala Ala Tyr Leu Pro Arg Met Trp Val Glu Lys His Pro Glu Lys Glu
 850 855 860

Ser Glu Ala Cys Met Leu Val Phe Gln Pro Asp Leu Asp Val Asp Leu
 865 870 875 880

Pro Asp Leu Ala Ser Glu Ser Glu Val Ile Ile Cys Leu Asp Cys Ser
 885 890 895

Ser Ser Met Glu Gly Val Thr Phe Leu Gln Ala Lys Gln Ile Thr Leu
 900 905 910

His Ala Leu Ser Leu Val Gly Glu Lys Gln Lys Val Asn Ile Ile Gln

915	920	925
Phe Gly Thr Gly Tyr Lys Glu Leu Phe Ser Tyr Pro Lys His Ile Thr 930 935 940		
Ser Asn Thr Thr Ala Ala Glu Phe Ile Met Ser Ala Thr Pro Thr Met 945 950 955 960		
Gly Asn Thr Asp Phe Trp Lys Thr Leu Arg Tyr Leu Ser Leu Leu Tyr 965 970 975		
Pro Ala Arg Gly Ser Arg Asn Ile Leu Leu Val Ser Asp Gly His Leu 980 985 990		
Gln Asp Glu Ser Leu Thr Leu Gln Leu Val Lys Arg Ser Arg Pro His 995 1000 1005		
Thr Arg Leu Phe Ala Cys Gly Ile Gly Ser Thr Ala Asn Arg His 1010 1015 1020		
Val Leu Arg Ile Leu Ser Gln Cys Gly Ala Gly Val Phe Glu Tyr 1025 1030 1035		
Phe Asn Ala Lys Ser Lys His Ser Trp Arg Lys Gln Ile Glu Asp 1040 1045 1050		
Gln Met Thr Arg Leu Cys Ser Pro Ser Cys His Ser Val Ser Val 1055 1060 1065		
Lys Trp Gln Gln Leu Asn Pro Asp Ala Pro Glu Ala Leu Gln Ala 1070 1075 1080		
Pro Ala Gln Val Pro Ser Leu Phe Arg Asn Asp Arg Leu Leu Val 1085 1090 1095		
Tyr Gly Phe Ile Pro His Cys Thr Gln Ala Thr Leu Cys Ala Leu 1100 1105 1110		
Ile Gln Glu Lys Glu Phe Cys Thr Met Val Ser Thr Thr Glu Leu 1115 1120 1125		
Gln Lys Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg Ala 1130 1135 1140		

Leu Ile	Arg Asp Tyr Glu Asp	Gly Ile Leu His Glu	Asn Glu Thr
1145	1150	1155	
Ser His	Glu Met Lys Lys Gln	Thr Leu Lys Ser Leu	Ile Ile Lys
1160	1165	1170	
Leu Ser	Lys Glu Asn Ser Leu	Ile Thr Gln Phe Thr	Ser Phe Val
1175	1180	1185	
Ala Val	Glu Lys Arg Asp Glu	Asn Glu Ser Pro Phe	Pro Asp Ile
1190	1195	1200	
Pro Lys	Val Ser Glu Leu Ile	Ala Lys Glu Asp Val	Asp Phe Leu
1205	1210	1215	
Pro Tyr	Met Ser Trp Gln Gly	Glu Pro Gln Glu Ala	Val Arg Asn
1220	1225	1230	
Gln Ser	Leu Leu Ala Ser Ser	Glu Trp Pro Glu Leu	Arg Leu Ser
1235	1240	1245	
Lys Arg	Lys His Arg Lys Ile	Pro Phe Ser Lys Arg	Lys Met Glu
1250	1255	1260	
Leu Ser	Gln Pro Glu Val Ser	Glu Asp Phe Glu Glu	Asp Gly Leu
1265	1270	1275	
Gly Val	Leu Pro Ala Phe Thr	Ser Asn Leu Glu Arg	Gly Gly Val
1280	1285	1290	
Glu Lys	Leu Leu Asp Leu Ser	Trp Thr Glu Ser Cys	Lys Pro Thr
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Ala Thr	Glu Pro Leu Phe Lys	Lys Val Ser Pro Trp	Glu Thr Ser
1310	1315	1320	
Thr Ser	Ser Phe Phe Pro Ile	Leu Ala Pro Ala Val	Gly Ser Tyr
1325	1330	1335	
Leu Thr	Pro Thr Thr Arg Ala	His Ser Pro Ala Ser	Leu Ser Phe
1340	1345	1350	
Ala Ser	Tyr Arg Gln Val Ala	Ser Phe Gly Ser Ala	Ala Pro Pro
1355	1360	1365	

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1370						1375					1380			
Thr	Cys	Ala	Asp	Trp	Ile	Pro	Gln	Ser	Ala	Ser	Cys	Pro	Thr	Gly
1385						1390					1395			
Pro	Pro	Gln	Asn	Pro	Pro	Ser	Ala	Pro	Tyr	Cys	Gly	Ile	Val	Phe
1400						1405					1410			
Ser	Gly	Ser	Ser	Leu	Ser	Ser	Ala	Gln	Ser	Ala	Pro	Leu	Gln	His
1415						1420					1425			
Pro	Gly	Gly	Phe	Thr	Thr	Arg	Pro	Ser	Ala	Gly	Thr	Phe	Pro	Glu
1430						1435					1440			
Leu	Asp	Ser	Pro	Gln	Leu	His	Phe	Ser	Leu	Pro	Thr	Asp	Pro	Asp
1445						1450					1455			
Pro	Ile	Arg	Gly	Phe	Gly	Ser	Tyr	His	Pro	Ser	Ala	Tyr	Ser	Pro
1460						1465					1470			
Phe	His	Phe	Gln	Pro	Ser	Ala	Ala	Ser	Leu	Thr	Ala	Asn	Leu	Arg
1475						1480					1485			
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1490						1495					1500			
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1505						1510					1515			
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1520						1525					1530			
Asp	Thr	Glu	Ser	Asp	Glu	Leu	Ser	Glu	Val	Leu	Gln	Asp	Ser	Cys
1535						1540					1545			
Phe	Leu	Gln	Ile	Lys	Cys	Asp	Thr	Lys	Asp	Asp	Ser	Ile	Pro	Cys
1550						1555					1560			
Phe	Leu	Glu	Leu	Lys	Glu	Glu	Asp	Glu	Ile	Val	Cys	Thr	Gln	His
1565						1570					1575			
Trp	Gln	Asp	Ala	Val	Pro	Trp	Thr	Glu	Leu	Leu	Ser	Leu	Gln	Thr

1580	1585	1590
Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu 1595	1600	1605
Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly 1610	1615	1620
Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu 1625	1630	1635
Ile Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu 1640	1645	1650
Lys Glu Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro 1655	1660	1665
Ser Ile Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln 1670	1675	1680
Ala Ser Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile 1685	1690	1695
Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys 1700	1705	1710
Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser Pro Leu His 1715	1720	1725
Arg Val Leu His Tyr Ser Gln Gly 1730	1735	

<210> 53

<211> 5211

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 53

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<210> 54
<211> 351
<212> PRT
<213> Artificial Sequence

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<220>

<223> *Saccaromyces cerevisiae* and *Homo sapiens*

<400> 54

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Gly Ile Pro Ala Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu
 100 105 110

Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu
 115 120 125

Glu Glu Ser Val Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala
 130 135 140

Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln
 145 150 155 160

Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile
 165 170 175

Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln
 180 185 190

His Trp Gln Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr
 195 200 205

Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn

210

215

220

Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln
 225 230 235 240

Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr
 245 250 255

Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile
 260 265 270

Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn
 275 280 285

Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg
 290 295 300

Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly
 305 310 315 320

Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile
 325 330 335

Ser Thr Val Ser Pro Leu His Arg Val Leu His Tyr Ser Gln Gly
 340 345 350

<210> 55

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Homo sapiens*

<400> 55

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tctcccaaaa caaaagggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180

ctagaaagac tggaacagct atttctactg attttctctc gagaagacct tgacatgatt 240

ttgaaaatgg attctttaca ggatataaaa gcattgttaa caggattagg aattcctgcc 300

aaccttaggc tgccaatggc ctctgcttta cctgaggctc tttgcagtca gtcccggact 360

accccgtag atctctgtct tctagaagaa tcagtaggca gtctcgaagg aagtcgatgt 420

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cctgtctttg cttttcaaag ttctgacaca gaaagtgatg agctatcaga agtacttcaa      480
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gaattaaaag aagaggatga aatagtgtgc acacaacact ggcaggatgc tgtgccttgg      600
acagaactcc tcagtctaca gacagaggat ggcttctgga aacttacacc agaactggga      660
cttatattaa atcttaatac aaatggtttg cacagctttc ttaaacaaaa aggcattcaa      720
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gaatgggtaa gaagaactga aggacagtac ccatctatct gccacgggt tgaactgggg      960
aacgactggg actctgccac caagcagttg ctgggactcc agcccataag cactgtgtcc     1020
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<210> 56

<211> 1820

<212> PRT

<213> Artificial Sequence

<220>

<223> Saccaromyces cerevisiae and Homo sapiens

<400> 56

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Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20              25              30

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35              40              45

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Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
50              55              60

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Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65              70              75              80

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Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85              90              95

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Met Val Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys Val Lys

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Asn Gly Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile 130 135 140		
Ile Leu Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile 145 150 155 160		
Gln Lys Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser 165 170 175		
Ile Arg Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys 180 185 190		
Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu 195 200 205		
Val Lys Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp 210 215 220		
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Leu Pro Gln Asp Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val 245 250 255		
Gly Met Glu Gly Gly Gln Glu Ala Val Val Val Glu Leu Gln Cys Ser 260 265 270		
Arg Asp Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu 275 280 285		
Asp Asp Gly Met Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser 290 295 300		
Glu Asp Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu Lys Lys 305 310 315 320		
Gln Gly Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr Gln Leu 325 330 335		

Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met Asn Ser
 340 345 350

Ser Thr Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile Trp Ala
 355 360 365

Glu Ala Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg
 370 375 380

Ile Ser Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val
 385 390 395 400

Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met
 405 410 415

Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys
 420 425 430

Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu
 435 440 445

Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn
 450 455 460

Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His
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Val Glu Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu
 485 490 495

Gln Asn His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg
 500 505 510

Val Gly Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn
 515 520 525

Val Arg Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile
 530 535 540

Leu Cys Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val
 545 550 555 560

Gln Arg Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp
 565 570 575

Ser Leu Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly
 580 585 590

Thr Arg Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp
 595 600 605

Leu His Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp
 610 615 620

Ser Val His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu
 625 630 635 640

Asp Asp Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr
 645 650 655

Ile Ile Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro
 660 665 670

Ser Asp His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe
 675 680 685

Ser Lys Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser
 690 695 700

Thr Lys Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu
 705 710 715 720

Asp Val His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile
 725 730 735

Val Phe Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys
 740 745 750

Tyr Ile Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala
 755 760 765

Phe Ile Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu
 770 775 780

Ala Gln Gln Glu Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr
 785 790 795 800

Leu Met Ser Gln Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn

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Ala Pro Trp Gln Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln Asp Thr		
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Val Glu Lys Ile Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser		
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Leu Thr Met Ser Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser		
885	890	895
Asp Thr His Glu Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val Ile		
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Ser Thr Met Glu Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser Leu His		
915	920	925
Ile Gly Leu Ser Ala Ala Tyr Leu Pro Arg Met Trp Val Glu Lys His		
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Asp Val Asp Leu Pro Asp Leu Ala Ser Glu Ser Glu Val Ile Ile Cys		
965	970	975
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Gln Ile Thr Leu His Ala Leu Ser Leu Val Gly Glu Lys Gln Lys Val		
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Asn Ile Ile Gln Phe Gly Thr Gly Tyr Lys Glu Leu Phe Ser Tyr		
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Pro Lys His Ile Thr Ser Asn Thr Thr Ala Ala Glu Phe Ile Met		
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Gln	Leu	Val	Lys	Arg	Ser	Arg	Pro	His	Thr	Arg	Leu	Phe	Ala	Cys
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His	Ser	Trp	Arg	Lys	Gln	Ile	Glu	Asp	Gln	Met	Thr	Arg	Leu	Cys
1130						1135					1140			
Ser	Pro	Ser	Cys	His	Ser	Val	Ser	Val	Lys	Trp	Gln	Gln	Leu	Asn
1145						1150					1155			
Pro	Asp	Ala	Pro	Glu	Ala	Leu	Gln	Ala	Pro	Ala	Gln	Val	Pro	Ser
1160						1165					1170			
Leu	Phe	Arg	Asn	Asp	Arg	Leu	Leu	Val	Tyr	Gly	Phe	Ile	Pro	His
1175						1180					1185			
Cys	Thr	Gln	Ala	Thr	Leu	Cys	Ala	Leu	Ile	Gln	Glu	Lys	Glu	Phe
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Cys	Thr	Met	Val	Ser	Thr	Thr	Glu	Leu	Gln	Lys	Thr	Thr	Gly	Thr
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Asp	Gly	Ile	Leu	His	Glu	Asn	Glu	Thr	Ser	His	Glu	Met	Lys	Lys
1235						1240					1245			
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 Ser Glu Trp Pro Glu Leu Arg Leu Ser Lys Arg Lys His Arg Lys
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 Ile Pro Phe Ser Lys Arg Lys Met Glu Leu Ser Gln Pro Glu Val
 1340 1345 1350

 Ser Glu Asp Phe Glu Glu Asp Gly Leu Gly Val Leu Pro Ala Phe
 1355 1360 1365

 Thr Ser Asn Leu Glu Arg Gly Gly Val Glu Lys Leu Leu Asp Leu
 1370 1375 1380

 Ser Trp Thr Glu Ser Cys Lys Pro Thr Ala Thr Glu Pro Leu Phe
 1385 1390 1395

 Lys Lys Val Ser Pro Trp Glu Thr Ser Thr Ser Ser Phe Phe Pro
 1400 1405 1410

 Ile Leu Ala Pro Ala Val Gly Ser Tyr Leu Thr Pro Thr Thr Arg
 1415 1420 1425

 Ala His Ser Pro Ala Ser Leu Ser Phe Ala Ser Tyr Arg Gln Val
 1430 1435 1440

 Ala Ser Phe Gly Ser Ala Ala Pro Pro Arg Gln Phe Asp Ala Ser
 1445 1450 1455

 Gln Phe Ser Gln Gly Pro Val Pro Gly Thr Cys Ala Asp Trp Ile
 1460 1465 1470

 Pro Gln Ser Ala Ser Cys Pro Thr Gly Pro Pro Gln Asn Pro Pro

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Arg Pro Ser Ala Gly Thr Phe Pro Glu Leu Asp Ser Pro Gln Leu 1520 1525 1530		
His Phe Ser Leu Pro Thr Asp Pro Asp Pro Ile Arg Gly Phe Gly 1535 1540 1545		
Ser Tyr His Pro Ser Ala Tyr Ser Pro Phe His Phe Gln Pro Ser 1550 1555 1560		
Ala Ala Ser Leu Thr Ala Asn Leu Arg Leu Pro Met Ala Ser Ala 1565 1570 1575		
Leu Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro Val Asp 1580 1585 1590		
Leu Cys Leu Leu Glu Glu Ser Val Gly Ser Leu Glu Gly Ser Arg 1595 1600 1605		
Cys Pro Val Phe Ala Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu 1610 1615 1620		
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Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln Asp Ala Val Pro 1655 1660 1665		
Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe Trp Lys 1670 1675 1680		
Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn Gly 1685 1690 1695		

Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln Ser Leu Gly Val
 1700 1705 1710

Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val
 1715 1720 1725

Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe
 1730 1735 1740

Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile
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Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg
 1760 1765 1770

Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu
 1775 1780 1785

Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln
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Pro Ile Ser Thr Val Ser Pro Leu His Arg Val Leu His Tyr Ser
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Gln Gly
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<210> 57
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<210> 58
<211> 491
<212> PRT

<213> Artificial Sequence

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<223> synthesized and Homo sapiens

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Ala
 225 230 235 240

Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser
 245 250 255

Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val
 260 265 270

Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser
 275 280 285

Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys Phe
 290 295 300

Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu
 305 310 315 320

Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln Asp
 325 330 335

Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe
 340 345 350

Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn
 355 360 365

Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln Ser Leu Gly Val
 370 375 380

Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val Leu
 385 390 395 400

Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe Lys Ser
 405 410 415

Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala
 420 425 430

Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg Arg Thr Glu Gly
 435 440 445

Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp
 450 455 460

Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser
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Pro Leu His Arg Val Leu His Tyr Ser Gln Gly
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<210> 59

<211> 1476

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

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<210> 60

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<223> synthesized and Homo sapiens

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20           25           30

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35           40           45

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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50           55           60

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Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65           70           75           80

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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85           90           95

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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115          120          125

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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn

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Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val				
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Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro				
	180		185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser				
	195		200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val				
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Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Met Val				
	225		230	235 240
Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys Val Lys Tyr Leu				
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Pro Gln Gln Gln Lys Lys Lys Leu Gln Thr Asp Ile Lys Glu Asn Gly				
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Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile Ile Leu				
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Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile Gln Lys				
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Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser Ile Arg				
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Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys Pro Leu				
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Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu Val Lys				
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Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp Thr Val				
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Gln Asp Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val Gly Met
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Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu Asp Asp
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 485 490 495

Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile Trp Ala Glu Ala
 500 505 510

Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg Ile Ser
 515 520 525

Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val Lys Ala
 530 535 540

Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met Met Thr
 545 550 555 560

Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys Glu Val
 565 570 575

Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu Ile Arg
 580 585 590

Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn Pro Pro
 595 600 605

Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His Val Glu
610 615 620

Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu Gln Asn
625 630 635 640

His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg Val Gly
645 650 655

Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn Val Arg
660 665 670

Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile Leu Cys
675 680 685

Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val Gln Arg
690 695 700

Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp Ser Leu
705 710 715 720

Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly Thr Arg
725 730 735

Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp Leu His
740 745 750

Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp Ser Val
755 760 765

His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu Asp Asp
770 775 780

Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr Ile Ile
785 790 795 800

Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro Ser Asp
805 810 815

His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe Ser Lys
820 825 830

Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser Thr Lys

835	840	845
Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu Asp Val		
850	855	860
His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile Val Phe		
865	870	875
Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys Tyr Ile		
885	890	895
Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala Phe Ile		
900	905	910
Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu Ala Gln		
915	920	925
Gln Glu Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr Leu Met		
930	935	940
Ser Gln Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn Leu Pro		
945	950	955
Pro Lys Ala Lys Val Leu Ile Lys Ile Thr Tyr Ile Thr Glu Leu Ser		
965	970	975
Ile Leu Gly Thr Val Gly Val Phe Phe Met Pro Ala Thr Val Ala Pro		
980	985	990
Trp Gln Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln Asp Thr Val Glu		
995	1000	1005
Lys Ile Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser Leu		
1010	1015	1020
Thr Met Ser Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser		
1025	1030	1035
Asp Thr His Glu Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val		
1040	1045	1050
Ile Ser Thr Met Glu Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser		
1055	1060	1065

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Val Lys Trp Gln Gln Leu Asn Pro Asp Ala Pro Glu Ala Leu Gln
 1295 1300 1305

 Ala Pro Ala Gln Val Pro Ser Leu Phe Arg Asn Asp Arg Leu Leu
 1310 1315 1320

 Val Tyr Gly Phe Ile Pro His Cys Thr Gln Ala Thr Leu Cys Ala
 1325 1330 1335

 Leu Ile Gln Glu Lys Glu Phe Cys Thr Met Val Ser Thr Thr Glu
 1340 1345 1350

 Leu Gln Lys Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg
 1355 1360 1365

 Ala Leu Ile Arg Asp Tyr Glu Asp Gly Ile Leu His Glu Asn Glu
 1370 1375 1380

 Thr Ser His Glu Met Lys Lys Gln Thr Leu Lys Ser Leu Ile Ile
 1385 1390 1395

 Lys Leu Ser Lys Glu Asn Ser Leu Ile Thr Gln Phe Thr Ser Phe
 1400 1405 1410

 Val Ala Val Glu Lys Arg Asp Glu Asn Glu Ser Pro Phe Pro Asp
 1415 1420 1425

 Ile Pro Lys Val Ser Glu Leu Ile Ala Lys Glu Asp Val Asp Phe
 1430 1435 1440

 Leu Pro Tyr Met Ser Trp Gln Gly Glu Pro Gln Glu Ala Val Arg
 1445 1450 1455

 Asn Gln Ser Leu Leu Ala Ser Ser Glu Trp Pro Glu Leu Arg Leu
 1460 1465 1470

 Ser Lys Arg Lys His Arg Lys Ile Pro Phe Ser Lys Arg Lys Met
 1475 1480 1485

 Glu Leu Ser Gln Pro Glu Val Ser Glu Asp Phe Glu Glu Asp Gly
 1490 1495 1500

 Leu Gly Val Leu Pro Ala Phe Thr Ser Asn Leu Glu Arg Gly Val

1505	1510	1515
Glu Lys Leu Leu Asp Leu Ser Trp Thr Glu Ser Cys Lys Pro Thr 1520 1525 1530		
Ala Thr Glu Pro Leu Phe Lys Lys Val Ser Pro Trp Glu Thr Ser 1535 1540 1545		
Thr Ser Ser Phe Phe Pro Ile Leu Ala Pro Ala Val Gly Ser Tyr 1550 1555 1560		
Leu Thr Pro Thr Thr Arg Ala His Ser Pro Ala Ser Leu Ser Phe 1565 1570 1575		
Ala Ser Tyr Arg Gln Val Ala Ser Phe Gly Ser Ala Ala Pro Pro 1580 1585 1590		
Arg Gln Phe Asp Ala Ser Gln Phe Ser Gln Gly Pro Val Pro Gly 1595 1600 1605		
Thr Cys Ala Asp Trp Ile Pro Gln Ser Ala Ser Cys Pro Thr Gly 1610 1615 1620		
Pro Pro Gln Asn Pro Pro Ser Ala Pro Tyr Cys Gly Ile Val Phe 1625 1630 1635		
Ser Gly Ser Ser Leu Ser Ser Ala Gln Ser Ala Pro Leu Gln His 1640 1645 1650		
Pro Gly Gly Phe Thr Thr Arg Pro Ser Ala Gly Thr Phe Pro Glu 1655 1660 1665		
Leu Asp Ser Pro Gln Leu His Phe Ser Leu Pro Thr Asp Pro Asp 1670 1675 1680		
Pro Ile Arg Gly Phe Gly Ser Tyr His Pro Ser Ala Tyr Ser Pro 1685 1690 1695		
Phe His Phe Gln Pro Ser Ala Ala Ser Leu Thr Ala Asn Leu Arg 1700 1705 1710		
Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser 1715 1720 1725		

Arg Thr	Thr Pro Val Asp	Leu Cys Leu Leu Glu Glu	Ser Val Gly
1730		1735	1740
Ser Leu	Glu Gly Ser Arg Cys	Pro Val Phe Ala Phe	Gln Ser Ser
1745		1750	1755
Asp Thr	Glu Ser Asp Glu Leu	Ser Glu Val Leu Gln	Asp Ser Cys
1760		1765	1770
Phe Leu	Gln Ile Lys Cys Asp	Thr Lys Asp Asp Ser	Ile Pro Cys
1775		1780	1785
Phe Leu	Glu Leu Lys Glu Glu	Asp Glu Ile Val Cys	Thr Gln His
1790		1795	1800
Trp Gln	Asp Ala Val Pro Trp	Thr Glu Leu Leu Ser	Leu Gln Thr
1805		1810	1815
Glu Asp	Gly Phe Trp Lys Leu	Thr Pro Glu Leu Gly	Leu Ile Leu
1820		1825	1830
Asn Leu	Asn Thr Asn Gly Leu	His Ser Phe Leu Lys	Gln Lys Gly
1835		1840	1845
Ile Gln	Ser Leu Gly Val Lys	Gly Arg Glu Cys Leu	Leu Asp Leu
1850		1855	1860
Ile Ala	Thr Met Leu Val Leu	Gln Phe Ile Arg Thr	Arg Leu Glu
1865		1870	1875
Lys Glu	Gly Ile Val Phe Lys	Ser Leu Met Lys Met	Asp Asp Pro
1880		1885	1890
Ser Ile	Ser Arg Asn Ile Pro	Trp Ala Phe Glu Ala	Ile Lys Gln
1895		1900	1905
Ala Ser	Glu Trp Val Arg Arg	Thr Glu Gly Gln Tyr	Pro Ser Ile
1910		1915	1920
Cys Pro	Arg Leu Glu Leu Gly	Asn Asp Trp Asp Ser	Ala Thr Lys
1925		1930	1935
Gln Leu	Leu Gly Leu Gln Pro	Ile Ser Thr Val Ser	Pro Leu His
1940		1945	1950

Arg Val Leu His Tyr Ser Gln Gly
1955 1960

<210> 61
<211> 5889
<212> DNA
<213> Artificial Sequence

<220>
<223> synthesized and Homo sapiens

<400> 61
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aagctcaccg tgaaattcat ctgcaccact ggaaagctcc ctgtgccatg gccaacactg 180
gtcactacct tcacctatgg cgtgcagtgc ttttcagat acccagacca tatgaagcag 240
catgactttt tcaagagcgc catgcccagag ggctatgtgc aggagagAAC catctttttc 300
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<210> 62

<211> 385

<212> PRT

<213> Artificial Sequence

<220>

<223> Levivirus and Homo sapiens

<400> 62

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser

35

40

45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr Gly Ile Pro Ala Asn Leu Arg Leu Pro Met Ala Ser Ala Leu
 130 135 140

Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro Val Asp Leu Cys
 145 150 155 160

Leu Leu Glu Glu Ser Val Gly Ser Leu Glu Gly Ser Arg Cys Pro Val
 165 170 175

Phe Ala Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu Leu Ser Glu Val
 180 185 190

Leu Gln Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp
 195 200 205

Ser Ile Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp Glu Ile Val Cys
 210 215 220

Thr Gln His Trp Gln Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu
 225 230 235 240

Gln Thr Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile
 245 250 255

Leu Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly
 260 265 270

Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile
 275 280 285

Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu
 290 295 300

Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser
 305 310 315 320

Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp
 325 330 335

Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu
 340 345 350

Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln
 355 360 365

Pro Ile Ser Thr Val Ser Pro Leu His Arg Val Leu His Tyr Ser Gln
 370 375 380

Gly
 385

<210> 63
 <211> 1158
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens

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cattacagtc aaggctaa                                     1158

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<210> 64

<211> 1854

<212> PRT

<213> Artificial Sequence

<220>

<223> Levivirus and Homo sapiens

<400> 64

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Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
                20              25              30

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Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
          35              40              45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
          50              55              60

```

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65              70              75              80

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Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
          85              90              95

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Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu

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Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly		
115	120	125
Ile Tyr Met Val Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys		
130	135	140
Val Lys Tyr Leu Pro Gln Gln Gln Lys Lys Lys Leu Gln Thr Asp Ile		
145	150	155
Lys Glu Asn Gly Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr		
165	170	175
His Ile Ile Leu Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn		
180	185	190
Ser Ile Gln Lys Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp		
195	200	205
Lys Ser Ile Arg Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro		
210	215	220
Tyr Lys Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser		
225	230	235
Ser Glu Val Lys Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu		
245	250	255
Glu Asp Thr Val Glu Leu Thr Glu Phe Gly Met Gln Asn Val Glu Ile		
260	265	270
Pro His Leu Pro Gln Asp Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu		
275	280	285
Lys Val Gly Met Glu Gly Gly Gln Glu Ala Val Val Val Glu Leu Gln		
290	295	300
Cys Ser Arg Asp Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe		
305	310	315
Leu Leu Asp Asp Gly Met Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys		
325	330	335

Thr Ser Glu Asp Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu
 340 345 350

Lys Lys Gln Gly Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr
 355 360 365

Gln Leu Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met
 370 375 380

Asn Ser Ser Thr Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile
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Trp Ala Glu Ala Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val
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Asn Arg Ile Ser Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu
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Leu Val Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln
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Lys Met Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met
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Pro Lys Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys
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Gln Leu Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys
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Pro Asn Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile
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Gly Asn Val Arg Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val
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Gly Ile Leu Cys Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg
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Gly Val Gln Arg Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe
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Asp Gly Thr Arg Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys
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Met Asp Leu His Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly
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Tyr Asp Ser Val His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp
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Phe Glu Asp Asp Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met
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Lys Tyr Ile Ile Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe
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His Pro Ser Asp His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser
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Asn Phe Ser Lys Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser
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Ser Ser Thr Lys Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro
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Leu Glu Asp Val His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln
 755 760 765

Val Ile Val Phe Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu
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Ala Lys Tyr Ile Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe
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Glu Ala Phe Ile Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys

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Phe Ser Leu Thr Met Ser Ile Glu Met Pro Tyr Val Ile Glu Phe Ile		
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Phe Ser Asp Thr His Glu Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala		
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Gln Ala Lys Gln Ile Thr Leu His Ala Leu Ser Leu Val Gly Glu		
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Thr	Arg	Leu	Cys	Ser	Pro	Ser	Cys	His	Ser	Val	Ser	Val	Lys	Trp
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Gln	Gln	Leu	Asn	Pro	Asp	Ala	Pro	Glu	Ala	Leu	Gln	Ala	Pro	Ala
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Gln	Val	Pro	Ser	Leu	Phe	Arg	Asn	Asp	Arg	Leu	Leu	Val	Tyr	Gly
1205						1210					1215			
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Glu Lys	Arg Asp Glu Asn Glu	Ser Pro Phe Pro Asp	Ile Pro Lys
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Val Ser	Glu Leu Ile Ala Lys	Glu Asp Val Asp Phe	Leu Pro Tyr
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Pro Thr	Thr Arg Ala His Ser	Pro Ala Ser Leu Ser	Phe Ala Ser
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Gln Asn Pro Pro Ser Ala Pro Tyr Cys Gly Ile Val Phe Ser Gly				
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Gly Phe Thr Thr Arg Pro Ser Ala Gly Thr Phe Pro Glu Leu Asp				
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Ser Pro Gln Leu His Phe Ser Leu Pro Thr Asp Pro Asp Pro Ile				
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Arg Gly Phe Gly Ser Tyr His Pro Ser Ala Tyr Ser Pro Phe His				
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Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln				
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Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro
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Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu
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Leu His Tyr Ser Gln Gly
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Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
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Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
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Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
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Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
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Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
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Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
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Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
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Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
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Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
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Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
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Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
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catgccagag atcctatattt tggcaatcaa atcattccgg atactgcgat tttaagtgtt 720
gttccattcc atcacgggtt tggaatgtt actacactcg gatatttgat atgtggattt 780
cgagtcgtct taatgtatag atttgaagaa gagctgtttc tgaggagcct tcaggattac 840
aagattcaaa gtgcgctgct ggtgccaacc ctattctcct tcttcgcaa aagcactctg 900
attgacaaat acgatttatt taatttacac gaaattgctt ctggtggcgc tccccctctt 960
aaggaagtcg ggaagcgggt tgccaagagg ttccatctgc caggtatcag gcaaggatat 1020
gggctcactg agactacatc agctattctg attacacccg agggggatga taaaccgggc 1080
gcggtcggtt aagttgttcc attttttgaa gcgaagggtt tggaatccat cttgctccaa 1140
acgctgggcg ttaatcaaag aggcgaactg tgtgtgagag gtcctatgat tatgtccggt 1200
tatgtaaaca atccggaagc gaccaacgcc ttgattgaca aggatggatg gctacattct 1260
ggagacatag cttactggga cgaagacgaa cacttcttca tcgttgaccg cctgaagtct 1320
ctgattaagt acaaaggcta tcagggtggc cccgctgaat tggaatccat cttgctccaa 1380
caccccaaca tcttcgacgc aggtgtcgca ggtcttcccg acgatgacgc cgggtgaactt 1440
cccgcgcgcg ttgttgtttt ggagcacgga aagacgatga cggaaaaaga gatcgtggat 1500
tacgtcgcca gtcaagtaac aaccgcgaaa aagttgcgcg gaggagttgt gtttgtggac 1560
gaagtaccga aaggtcttac cggaaaactc gacgcaagaa aaatcagaga gatcctcata 1620
aaggccaaga agggcggaaa gatcgccgtg gtaa 1654

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<210> 68
 <211> 805
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> *Photinus pyralis* and *Homo sapiens*

<400> 68

Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
 1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
 35 40 45
 Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
 50 55 60
 Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
 65 70 75 80
 Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
 85 90 95
 Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
 100 105 110
 Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
 115 120 125
 Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
 130 135 140
 Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
 145 150 155 160
 Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
 165 170 175
 Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
 180 185 190
 Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
 195 200 205
 Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp
 210 215 220
 Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
 225 230 235 240
 Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
 245 250 255
 Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
 260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
 275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
 290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
 305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
 325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
 340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
 355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu

500	505	510
Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly		
515	520	525
Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys		
530	535	540
Gly Gly Lys Ile Ala Val Gly Ile Pro Ala Asn Leu Arg Leu Pro Met		
545	550	555 560
Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro		
	565	570 575
Val Asp Leu Cys Leu Leu Glu Glu Ser Val Gly Ser Leu Glu Gly Ser		
	580	585 590
Arg Cys Pro Val Phe Ala Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu		
	595	600 605
Leu Ser Glu Val Leu Gln Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp		
	610	615 620
Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp		
	625	630 635 640
Glu Ile Val Cys Thr Gln His Trp Gln Asp Ala Val Pro Trp Thr Glu		
	645	650 655
Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu		
	660	665 670
Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu		
	675	680 685
Lys Gln Lys Gly Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu		
	690	695 700
Leu Asp Leu Ile Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg		
	705	710 715 720
Leu Glu Lys Glu Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp		
	725	730 735

Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln
 740 745 750

Ala Ser Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys
 755 760 765

Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu
 770 775 780

Leu Gly Leu Gln Pro Ile Ser Thr Val Ser Pro Leu His Arg Val Leu
 785 790 795 800

His Tyr Ser Gln Gly
 805

<210> 69
 <211> 2418
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Photinus pyralis and Homo sapiens

<400> 69
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 accgctggag agcaactgca taaggctatg aagagatacg ccctgggttc tggaacaatt 120
 gcttttacag atgcacatat cgaggtggac atcacttacg ctgagtactt cgaaatgtcc 180
 gttcgggttg cagaagctat gaaacgatat gggctgaata caaatcacag aatcgtcgta 240
 tgcagtgaaa actctcttca attctttatg ccggtgttg gcgcgttatt tatcggagtt 300
 gcagttgcgc ccgcgaacga catttataat gaacgtgaat tgctcaacag tatgggcatt 360
 tcgcagccta ccgtggtggt cgtttccaaa aaggggttgc aaaaaatttt gaacgtgcaa 420
 aaaaagctcc caatcatcca aaaaattatt atcatggatt ctaaaacgga ttaccaggga 480
 tttcagtcga tgtacacggt cgtcacatct catctacctc ccggttttaa tgaatacgat 540
 tttgtgccag agtccttcga tagggacaag acaattgcac tgatcatgaa ctccctctgga 600
 tctactgggtc tgcctaaagg tgctgctctg cctcatagaa ctgcctgcgt gagattctcg 660
 catgccagag atcctatttt tggcaatcaa atcattccgg atactgcgat ttttaagtgtt 720
 gttccattcc atcacggttt tggaatgttt actacactcg gatatttgat atgtggattt 780
 cgagtcgtct taatgtatag atttgaagaa gagctgtttc tgaggagcct tcaggattac 840
 aagattcaaa gtgcgctgct ggtgccaacc ctattctcct tcttcgcaa aagcactctg 900

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attgacaaat acgatttatc taattttacac gaaattgctt ctggtggcgc tcccctctct 960
aaggaagtcg gggaagcggg tgccaagagg ttccatctgc caggtatcag gcaaggatat 1020
gggctcactg agactacatc agctattctg attacacccg agggggatga taaaccgggc 1080
gcggtcggta aagttgttcc attttttgaa gcgaagggtg tggatctgga taccgggaaa 1140
acgctgggcg ttaatcaaag aggcgaaactg tgtgtgagag gtcctatgat tatgtccggt 1200
tatgtaaaca atccggaagc gaccaacgcc ttgattgaca aggatggatg gctacattct 1260
ggagacatag cttactggga cgaagacgaa cacttcttca tcgttgaccg cctgaagtct 1320
ctgattaagt acaaaggcta tcagggtggc cccgctgaat tggaatccat cttgctccaa 1380
caccccaaca tcttcgacgc aggtgtcgcg ggtcttcccg acgatgacgc cggatgaactt 1440
cccgccgccc ttgttgtttt ggagcacgga aagacgatga cggaaaaaga gatcgtggat 1500
tacgtcgcca gtcaagtaac aaccgcgaaa aagttgcgcg gaggagtgtg gtttgtggac 1560
gaagtaccga aaggtcttac cggaaaactc gacgcaagaa aaatcagaga gatcctcata 1620
aaggccaaga agggcggaag gatcgccgtg ggaattcctg ccaaccttag gctgccaatg 1680
gcctctgctt tacctgaggc tctttgcagt cagtcccgga ctaccccgat agatctctgt 1740
cttctagaag aatcagtagg cagtctcgaa ggaagtogat gtccgtgtct tgcttttcaa 1800
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ataaagtgtg atacaaaaga tgacagtatc ccgtgctttc tggaattaaa agaagaggat 1920
gaaatagtgt gcacacaaca ctggcaggat gctgtgcctt ggacagaact cctcagtcta 1980
cagacagagg atggcttctg gaaacttaca ccagaactgg gacttatatt aaatcttaat 2040
acaaatgggt tgcacagctt tcttaaacia aaaggcattc aatctctagg tgtaaaagga 2100
agagaatgtc tcctggacct aattgccaca atgctggtac tacagtttat tcgcaccagg 2160
ttggaaaaag agggaaatagt gttcaaata ctgatgaaaa tggatgacct ttctatttcc 2220
aggaatatte cctgggcttt tgaggcaata aagcaagcaa gtgaatgggt aagaagaact 2280
gaaggacagt accatctat ctgcccacgg cttgaactgg ggaacgactg ggactctgcc 2340
accaagcagt tgctgggact ccagcccata agcactgtgt cccctcttca tagagtctc 2400
cattacagtc aaggctaa 2418

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<210> 70
 <211> 2274
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Photinus pyralis and Homo sapiens

<400> 70

Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
 1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
 35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
 50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
 65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
 85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
 100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
 115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
 130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
 145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
 165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
 180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
 195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp

210	215	220
Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val		
225	230	235 240
Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu		
	245	250 255
Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu		
	260	265 270
Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val		
	275	280 285
Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr		
	290	295 300
Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser		
305	310	315 320
Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile		
	325	330 335
Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr		
	340	345 350
Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe		
	355	360 365
Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val		
	370	375 380
Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly		
385	390	395 400
Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly		
	405	410 415
Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe		
	420	425 430
Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln		
	435	440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
 500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
 530 535 540

Gly Gly Lys Ile Ala Val Met Val Met Gly Ile Phe Ala Asn Cys Ile
 545 550 555 560

Phe Cys Leu Lys Val Lys Tyr Leu Pro Gln Gln Gln Lys Lys Lys Leu
 565 570 575

Gln Thr Asp Ile Lys Glu Asn Gly Gly Lys Phe Ser Phe Ser Leu Asn
 580 585 590

Pro Gln Cys Thr His Ile Ile Leu Asp Asn Ala Asp Val Leu Ser Gln
 595 600 605

Tyr Gln Leu Asn Ser Ile Gln Lys Asn His Val His Ile Ala Asn Pro
 610 615 620

Asp Phe Ile Trp Lys Ser Ile Arg Glu Lys Arg Leu Leu Asp Val Lys
 625 630 635 640

Asn Tyr Asp Pro Tyr Lys Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln
 645 650 655

Lys Ala Ser Ser Ser Glu Val Lys Thr Glu Gly Leu Cys Pro Asp Ser
 660 665 670

Ala Thr Glu Glu Glu Asp Thr Val Glu Leu Thr Glu Phe Gly Met Gln
 675 680 685

Asn Val Glu Ile Pro His Leu Pro Gln Asp Phe Glu Val Ala Lys Tyr
 690 695 700

Asn Thr Leu Glu Lys Val Gly Met Glu Gly Gly Gln Glu Ala Val Val
 705 710 715 720

Val Glu Leu Gln Cys Ser Arg Asp Ser Arg Asp Cys Pro Phe Leu Ile
 725 730 735

Ser Ser His Phe Leu Leu Asp Asp Gly Met Glu Thr Arg Arg Gln Phe
 740 745 750

Ala Ile Lys Lys Thr Ser Glu Asp Ala Ser Glu Tyr Phe Glu Asn Tyr
 755 760 765

Ile Glu Glu Leu Lys Lys Gln Gly Phe Leu Leu Arg Glu His Phe Thr
 770 775 780

Pro Glu Ala Thr Gln Leu Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu
 785 790 795 800

Glu Glu Val Met Asn Ser Ser Thr Leu Ser Gln Glu Val Ser Asp Leu
 805 810 815

Val Glu Met Ile Trp Ala Glu Ala Leu Gly His Leu Glu His Met Leu
 820 825 830

Leu Lys Pro Val Asn Arg Ile Ser Leu Asn Asp Val Ser Lys Ala Glu
 835 840 845

Gly Ile Leu Leu Leu Val Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala
 850 855 860

Glu Gln Leu Gln Lys Met Met Thr Glu Phe Tyr Arg Leu Ile Pro His
 865 870 875 880

Lys Gly Thr Met Pro Lys Glu Val Asn Leu Gly Leu Leu Ala Lys Lys
 885 890 895

Ala Asp Leu Cys Gln Leu Ile Arg Asp Met Val Asn Val Cys Glu Thr
 900 905 910

Asn Leu Ser Lys Pro Asn Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu

915	920	925
Arg Cys Lys Ile Glu His Val Glu Gln Asn Thr Glu Glu Phe Leu Arg		
930	935	940
Val Arg Lys Glu Val Leu Gln Asn His His Ser Lys Ser Pro Val Asp		
945	950	955 960
Val Leu Gln Ile Phe Arg Val Gly Arg Val Asn Glu Thr Thr Glu Phe		
	965	970 975
Leu Ser Lys Leu Gly Asn Val Arg Pro Leu Leu His Gly Ser Pro Val		
	980	985 990
Gln Asn Ile Val Gly Ile Leu Cys Arg Gly Leu Leu Leu Pro Lys Val		
	995	1000 1005
Val Glu Asp Arg Gly Val Gln Arg Thr Asp Val Gly Asn Leu Gly		
	1010	1015 1020
Ser Gly Ile Tyr Phe Ser Asp Ser Leu Ser Thr Ser Ile Lys Tyr		
	1025	1030 1035
Ser His Pro Gly Glu Thr Asp Gly Thr Arg Leu Leu Leu Ile Cys		
	1040	1045 1050
Asp Val Ala Leu Gly Lys Cys Met Asp Leu His Glu Lys Asp Phe		
	1055	1060 1065
Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp Ser Val His Gly Val		
	1070	1075 1080
Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu Asp Asp Glu Phe		
	1085	1090 1095
Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr Ile Ile Lys		
	1100	1105 1110
Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro Ser Asp		
	1115	1120 1125
His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe Ser		
	1130	1135 1140

Lys Val	Glu Asp Tyr Gln Leu	Pro Asp Ala Lys Thr	Ser Ser Ser
1145	1150	1155	
Thr Lys	Ala Gly Leu Gln Asp	Ala Ser Gly Asn Leu	Val Pro Leu
1160	1165	1170	
Glu Asp	Val His Ile Lys Gly	Arg Ile Ile Asp Thr	Val Ala Gln
1175	1180	1185	
Val Ile	Val Phe Gln Thr Tyr	Thr Asn Lys Ser His	Val Pro Ile
1190	1195	1200	
Glu Ala	Lys Tyr Ile Phe Pro	Leu Asp Asp Lys Ala	Ala Val Cys
1205	1210	1215	
Gly Phe	Glu Ala Phe Ile Asn	Gly Lys His Ile Val	Gly Glu Ile
1220	1225	1230	
Lys Glu	Lys Glu Glu Ala Gln	Gln Glu Tyr Leu Glu	Ala Val Thr
1235	1240	1245	
Gln Gly	His Gly Ala Tyr Leu	Met Ser Gln Asp Ala	Pro Asp Val
1250	1255	1260	
Phe Thr	Val Ser Val Gly Asn	Leu Pro Pro Lys Ala	Lys Val Leu
1265	1270	1275	
Ile Lys	Ile Thr Tyr Ile Thr	Glu Leu Ser Ile Leu	Gly Thr Val
1280	1285	1290	
Gly Val	Phe Phe Met Pro Ala	Thr Val Ala Pro Trp	Gln Gln Asp
1295	1300	1305	
Lys Ala	Leu Asn Glu Asn Leu	Gln Asp Thr Val Glu	Lys Ile Cys
1310	1315	1320	
Ile Lys	Glu Ile Gly Thr Lys	Gln Ser Phe Ser Leu	Thr Met Ser
1325	1330	1335	
Ile Glu	Met Pro Tyr Val Ile	Glu Phe Ile Phe Ser	Asp Thr His
1340	1345	1350	
Glu Leu	Lys Gln Lys Arg Thr	Asp Cys Lys Ala Val	Ile Ser Thr
1355	1360	1365	

Met Glu Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser Leu His Ile
 1370 1375 1380

Gly Leu Ser Ala Ala Tyr Leu Pro Arg Met Trp Val Glu Lys His
 1385 1390 1395

Pro Glu Lys Glu Ser Glu Ala Cys Met Leu Val Phe Gln Pro Asp
 1400 1405 1410

Leu Asp Val Asp Leu Pro Asp Leu Ala Ser Glu Ser Glu Val Ile
 1415 1420 1425

Ile Cys Leu Asp Cys Ser Ser Ser Met Glu Gly Val Thr Phe Leu
 1430 1435 1440

Gln Ala Lys Gln Ile Thr Leu His Ala Leu Ser Leu Val Gly Glu
 1445 1450 1455

Lys Gln Lys Val Asn Ile Ile Gln Phe Gly Thr Gly Tyr Lys Glu
 1460 1465 1470

Leu Phe Ser Tyr Pro Lys His Ile Thr Ser Asn Thr Thr Ala Ala
 1475 1480 1485

Glu Phe Ile Met Ser Ala Thr Pro Thr Met Gly Asn Thr Asp Phe
 1490 1495 1500

Trp Lys Thr Leu Arg Tyr Leu Ser Leu Leu Tyr Pro Ala Arg Gly
 1505 1510 1515

Ser Arg Asn Ile Leu Leu Val Ser Asp Gly His Leu Gln Asp Glu
 1520 1525 1530

Ser Leu Thr Leu Gln Leu Val Lys Arg Ser Arg Pro His Thr Arg
 1535 1540 1545

Leu Phe Ala Cys Gly Ile Gly Ser Thr Ala Asn Arg His Val Leu
 1550 1555 1560

Arg Ile Leu Ser Gln Cys Gly Ala Gly Val Phe Glu Tyr Phe Asn
 1565 1570 1575

Ala Lys Ser Lys His Ser Trp Arg Lys Gln Ile Glu Asp Gln Met

1580		1585		1590
Thr Arg Leu Cys Ser Pro Ser Cys His Ser Val Ser Val Lys Trp				
1595		1600		1605
Gln Gln Leu Asn Pro Asp Ala Pro Glu Ala Leu Gln Ala Pro Ala				
1610		1615		1620
Gln Val Pro Ser Leu Phe Arg Asn Asp Arg Leu Leu Val Tyr Gly				
1625		1630		1635
Phe Ile Pro His Cys Thr Gln Ala Thr Leu Cys Ala Leu Ile Gln				
1640		1645		1650
Glu Lys Glu Phe Cys Thr Met Val Ser Thr Thr Glu Leu Gln Lys				
1655		1660		1665
Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg Ala Leu Ile				
1670		1675		1680
Arg Asp Tyr Glu Asp Gly Ile Leu His Glu Asn Glu Thr Ser His				
1685		1690		1695
Glu Met Lys Lys Gln Thr Leu Lys Ser Leu Ile Ile Lys Leu Ser				
1700		1705		1710
Lys Glu Asn Ser Leu Ile Thr Gln Phe Thr Ser Phe Val Ala Val				
1715		1720		1725
Glu Lys Arg Asp Glu Asn Glu Ser Pro Phe Pro Asp Ile Pro Lys				
1730		1735		1740
Val Ser Glu Leu Ile Ala Lys Glu Asp Val Asp Phe Leu Pro Tyr				
1745		1750		1755
Met Ser Trp Gln Gly Glu Pro Gln Glu Ala Val Arg Asn Gln Ser				
1760		1765		1770
Leu Leu Ala Ser Ser Glu Trp Pro Glu Leu Arg Leu Ser Lys Arg				
1775		1780		1785
Lys His Arg Lys Ile Pro Phe Ser Lys Arg Lys Met Glu Leu Ser				
1790		1795		1800

Gln	Pro	Glu	Val	Ser	Glu	Asp	Phe	Glu	Glu	Asp	Gly	Leu	Gly	Val
1805						1810					1815			
Leu	Pro	Ala	Phe	Thr	Ser	Asn	Leu	Glu	Arg	Gly	Gly	Val	Glu	Lys
1820						1825					1830			
Leu	Leu	Asp	Leu	Ser	Trp	Thr	Glu	Ser	Cys	Lys	Pro	Thr	Ala	Thr
1835						1840					1845			
Glu	Pro	Leu	Phe	Lys	Lys	Val	Ser	Pro	Trp	Glu	Thr	Ser	Thr	Ser
1850						1855					1860			
Ser	Phe	Phe	Pro	Ile	Leu	Ala	Pro	Ala	Val	Gly	Ser	Tyr	Leu	Thr
1865						1870					1875			
Pro	Thr	Thr	Arg	Ala	His	Ser	Pro	Ala	Ser	Leu	Ser	Phe	Ala	Ser
1880						1885					1890			
Tyr	Arg	Gln	Val	Ala	Ser	Phe	Gly	Ser	Ala	Ala	Pro	Pro	Arg	Gln
1895						1900					1905			
Phe	Asp	Ala	Ser	Gln	Phe	Ser	Gln	Gly	Pro	Val	Pro	Gly	Thr	Cys
1910						1915					1920			
Ala	Asp	Trp	Ile	Pro	Gln	Ser	Ala	Ser	Cys	Pro	Thr	Gly	Pro	Pro
1925						1930					1935			
Gln	Asn	Pro	Pro	Ser	Ala	Pro	Tyr	Cys	Gly	Ile	Val	Phe	Ser	Gly
1940						1945					1950			
Ser	Ser	Leu	Ser	Ser	Ala	Gln	Ser	Ala	Pro	Leu	Gln	His	Pro	Gly
1955						1960					1965			
Gly	Phe	Thr	Thr	Arg	Pro	Ser	Ala	Gly	Thr	Phe	Pro	Glu	Leu	Asp
1970						1975					1980			
Ser	Pro	Gln	Leu	His	Phe	Ser	Leu	Pro	Thr	Asp	Pro	Asp	Pro	Ile
1985						1990					1995			
Arg	Gly	Phe	Gly	Ser	Tyr	His	Pro	Ser	Ala	Tyr	Ser	Pro	Phe	His
2000						2005					2010			
Phe	Gln	Pro	Ser	Ala	Ala	Ser	Leu	Thr	Ala	Asn	Leu	Arg	Leu	Pro
2015						2020					2025			

Met Ala	Ser Ala Leu Pro	Glu Ala Leu Cys Ser	Gln Ser Arg Thr
2030		2035	2040
Thr Pro	Val Asp Leu Cys Leu	Leu Glu Glu Ser	Val Gly Ser Leu
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Glu Trp	Val Arg Arg Thr	Glu Gly Gln Tyr	Pro Ser Ile Cys Pro
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<400> 74

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Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
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Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
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Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
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Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
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Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
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agggtccaga aggtccgaga gctggaactg gtctatgccc gggcccagct ggagctggag 2340
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ctgctccagt ccctgggctt gaaatcaacc ctcatcaccg atgggtccac tcccatcaac 2520
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agggtggcca gtggggccag ccctggggag gggatatccc ccagttctgc tcaggcccct 2640
caagctcctg gagacaacca cgtggtgcct gtactgcgcc gacagatcaa gatctgggtt 2700
cagaacgcac ggatgaagtg gaagaagtga 2730

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<210> 76

<211> 877

<212> PRT

<213> Artificial Sequence

<220>

<223> Rattus norvegicus and Drosophila melanogaster

<400> 76

```

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10           15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
          20           25           30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
          35           40           45

```

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
          50           55           60

```

```

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
65           70           75           80

```

```

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
          85           90           95

```

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 340 345 350
 Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365
 Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 370 375 380
 Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400
 Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415
 Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 420 425 430
 Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 435 440 445
 Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460
 Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 465 470 475 480
 Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 485 490 495
 Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510
 Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525
 Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540
 Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 545 550 555 560
 Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala

	565		570		575
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His					
	580		585		590
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met					
	595		600		605
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp					
	610		615		620
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val					
	625		630		635
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg					
			645		650
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala					
	660		665		670
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu					
	675		680		685
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys					
	690		695		700
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly					
	705		710		715
Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu					
			725		730
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala					
	740		745		750
Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met					
	755		760		765
Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala					
	770		775		780
Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu					
	785		790		795
					800

252/429

gttgtcaagg gagagaagtc ctttttcctc cagccaggag agaggctgga gcgaggcatc 960
 caggatgtgt atgtgctgtc agagcagcag gggctgctac tgaaggcact gcagcccctg 1020
 gaggagggag agagcgagga gaaggctctcc catcaggccg gagactgctg gctcatccgt 1080
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 gtgattggaa gcacctacat gctgactcag gatgaagtcc tgtgggaaaa ggagctgcct 1260
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 gtgagcaagg cgcagcagct tgccaatgtg gaggcaaaga agttcaagga gatgacagag 2400
 gcactgggcc ccggcaccat caggacactg gctgtggccg ggccagagat gcaggtgaaa 2460
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 ctcttcagca cagccttcgg gttgctgggg ctggggtctg atggtcagcc gccagcacag 2580
 aagcgacaga tcaagatctg gtttcagaac gcacggatga agtgaagaa gtga 2634

<210> 78
 <211> 11
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 78

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1 5 10

<210> 79
 <211> 33
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 79

tacgggcgga agaagcggcg acagaggcga cgg

33

<210> 80
 <211> 904
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Homo sapiens and Human immunodeficiency virus type 1

<400> 80

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 1 5 10 15

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His

580	585	590
Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr 595 600 605		
Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp 610 615 620		
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 625 630 635 640		
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 645 650 655		
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 660 665 670		
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675 680 685		
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 690 695 700		
Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly 705 710 715 720		
Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu 725 730 735		
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala 740 745 750		
Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu 755 760 765		
Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala 770 775 780		
Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu 785 790 795 800		
Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu 805 810 815		

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Tyr Gly Arg
 885 890 895

Lys Lys Arg Arg Gln Arg Arg Arg
 900

<210> 81
 <211> 2715
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapiens and Human immunodeficiency virus type 1

<400> 81
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 gagagggtac tgtttgcccc catgcgcacg gtgaccgtcc ccccacgtca ctactgcaca 180
 gtggccaacc ctgtgtctcg ggatgccag ggcttggtgc tgtttgatgt cacagggcaa 240
 gttcggcttc gccacgctga cctcgagatc cggctggccc aggaccctt cccctgtac 300
 ccaggggagg tgctggaaaa ggacatcaca cccctgcagg tggttctgcc caacactgcc 360
 ctccatctaa aggcgctgct tgattttgag gataaagatg gagacaaggt ggtggcagga 420
 gatgagtggc ttttcgaggg acctggcacg tacatcccc ggaaggaagt ggaggtcgtg 480
 gagatcattc aggccaccat catcaggcag aaccaggctc tgcggctcag ggcccgaag 540
 gagtgtctgg accgggacgg caaggagagg gtgacagggg aagaatggct ggtcaccaca 600
 gtaggggctg acctcccagc ggtgtttgag gaggttctgg atttggtgga cgccgtcatc 660
 cttacggaaa agacagccct gcacctccgg gctcggcgga acttccggga cttcagggga 720
 gtgtcccgcc gcactgggga ggagtggctg gtaacagtgc aggacacaga ggcccacgtg 780

ccagatgtcc acgaggaggt gctggggggt gtgcccata ccaccctggg cccccacaac	840
tactgctga ttctcgaccc tgtcggaccg gatggcaaga atcagctggg gcagaagcgc	900
gtggtcaagg gagagaagtc ttttttcctc cagccaggag agcagctgga acaaggcatc	960
caggatgtgt atgtgctgtc ggagcagcag gggctgctgc tgagggccct gcagcccctg	1020
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ggacccttg agtatgtgcc atctgcaaaa gtggaggtgg tggaggagcg ccaggccatc	1140
cctctagacg agaacgaggg catctatgtg caggatgtca agaccggaaa ggtgcgcgct	1200
gtgattggaa gcacctacat gctgaccag gacgaagtcc tgtgggagaa agagctgcct	1260
cccgggggtg aggagctgct gaacaagggg caggaccctc tggcagacag gggtgagaag	1320
gacacagcta agagcctcca gcccttggcg ccccggaaca agaccctgtg ggtcagctac	1380
cgctgcccc acaacgctgc ggtgcagggt tacgactacc gagagaagcg agcccgctg	1440
gtcttcgggc ctgagctggt gtcgctgggt cctgaggagc agttcacagt gttgtccctc	1500
tcagctgggc ggcccaagcg tccccatgcc cgccgtgcgc tctgctgct gctggggcct	1560
gactttctca cagacgtcat caccatcgaa acggcggatc atgccaggct gcaactgcag	1620
ctggcctaca actggcactt tgagggtgaat gaccggaagg acccccaaga gacggccaag	1680
ctcttttcag tgccagactt tgtaggtgat gcctgcaaag ccatcgcatc ccgggtgcgg	1740
ggggccgtgg cctctgtcac ttctgatgac ttccataaga actcagcccc catcattcgc	1800
actgctgtct ttggctttga gacctcgaa gcgaagggcc ccgatggcat ggccctgccc	1860
aggccccggg accaggctgt cttcccccaa aacgggctgg tggtcagcag tgtggacgtg	1920
cagtcagtgg agcctgtgga tcagaggacc cgggacgccc tgcaacgcag cgtccagctg	1980
gccatcgaga tcaccaccaa ctcccaggaa gcggcggcca agcatgaggc tcagagactg	2040
gagcaggaag ccgcgggccg gcttgagcgg cagaagatcc tggaccagtc agaagccgag	2100
aaagctcgca aggaactttt ggagctggag gctctgagca tggccgtgga gagcaccggg	2160
actgccaagg cggaggccga gtcccgtgcg gaggcagccc ggattgaggg agaagggctc	2220
gtgctgcagg ccaagctaaa agcacaggcc ttggccattg aaacggaggc tgagctccag	2280
agggtccaga aggtccgaga gctggaactg gtctatgccc gggcccagct ggagctggag	2340
gtgagcaagg ctcagcagct ggctgaggtg gaggtgaaga agttcaagca gatgacagag	2400
gccataggcc ccagcaccat cagggaacct gctgtggctg ggcctgagat gcaggtaaaa	2460
ctgctccagt ccctgggcct gaaatcaacc ctcatcacc atggctccac tcccatcaac	2520

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ctctttcaaca cagccttttg gctgctgggg atggggcccg agggtcagcc cctgggcaga    2580
agggtggcca gtgggcccag ccctggggag gggatatccc ccagttctgc tcaggcccct    2640
caagctcctg gagacaacca cgtggtgcct gtactgcgct acgggcggaa gaagcggcga    2700
cagaggcgac ggtga                                                    2715

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<210> 82

<211> 872

<212> PRT

<213> Artificial Sequence

<220>

<223> Rattus norvegicus and Human immunodeficiency virus type 1

<400> 82 .

```

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10           15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
          20           25           30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
          35           40           45

```

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
          50           55           60

```

```

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
65           70           75           80

```

```

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
          85           90           95

```

```

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
          100          105          110

```

```

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
          115          120          125

```

```

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
          130          135          140

```

```

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
          145          150          155          160

```


Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
 595 600 605

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
 610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val

625		630		635		640
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg						
	645			650		655
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala						
	660			665		670
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu						
	675			680		685
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys						
	690			695		700
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly						
705		710		715		720
Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu						
	725			730		735
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala						
	740			745		750
Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met						
	755			760		765
Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala						
	770			775		780
Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu						
785		790		795		800
Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu						
	805			810		815
Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile						
	820			825		830
Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu						
	835			840		845
Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Tyr Gly Arg						
	850			855		860

Lys Lys Arg Arg Gln Arg Arg Arg
865 870

<210> 83
<211> 2619
<212> DNA
<213> Artificial Sequence

<220>
<223> Rattus norvegicus and Human immunodeficiency virus type 1

<400> 83
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gacgagtggc tatttgaggg acctggcacc tacatcccac agaaggaagt ggaagtcgtg 480
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gagtgccttg accgggaggg caaggggcgc gtgacaggtg aggagtggct ggtccgatcc 600
gtgggggctt acctcccagc tgtctttgaa gaggtgctgg atctggtgga tgctgtgatc 660
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tctgggggtg aggagctgct gaacttgggg catgaccctc tggcagacag gggtcagaag 1320
ggcacagcca agcccttca gccctcagct ccaaggaaca agaccgagt ggtcagctac 1380

```

cgtgtcccg c acaatgcagc ggtgcaggtc tatgactaca gagccaagag agcccggtgtg 1440
gtctttgggc c cgagctagt gacactggat cctgaggagc agttcacagt attgtccctt 1500
tctgccgggc g acccaagcg tcctcatgcc cgccgtgcac tctgcctact gctgggacct 1560
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cttctccagt ccctgggcct gaaatccact ctcatcaccg atggctcgtc tcccatcaac 2520
ctcttcagca cagccttcgg gttgctgggg ctggggctctg atggtcagcc gccagcacag 2580
aagtacgggc ggaagaagcg gcgacagagg cgacggtga 2619

```

<210> 84

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> completely synthesized

<400> 84

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe

```

20 25 30
 Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
 50 55 60
 Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp
 65 70 75 80
 Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
 85 90 95
 Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110
 Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly
 130 135 140
 Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp
 145 150 155 160
 Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp
 165 170 175

Ile Gly Arg

<210> 85
 <211> 747
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 85
 gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctcttgggca gagggccacc 60
 atgtcctgca gagccggtga aagtgttgat atttttggcg ttgggttttt gcaactggtac 120
 cagcagaaac caggacagcc acccaaactc ctcattctatc gtgcatccaa cctagaatct 180

```

gggatccctg tcagggttcag tggcactggg tctaggacag acttcaccct catcattgat      240
cctgtggagg ctgatgatgt tgccacctat tactgtcagc aaactaatga ggatccgtac      300
acgttcggag gggggaccaa gctggaaata aaaggcagta ctagcggcgg tggctccggg      360
ggcggttccg gtgggggagg cagcagcgag gttcagctac aacagtctgg ggcagagctt      420
gtggagccag gggcctcagt caagttgtcc tgcacagctt ctggcttcaa cattaaagac      480
acctatatgc actgggtgaa gcagaggcct gaacagggcc tggaatggat tggaaggatt      540
gatcctgcga atggtaatag taaatatgtc ccgaagttcc agggcaaggc cactataaca      600
gcagacacat cttccaacac agcctacctg cagctcacca gcctgacatc tgaggacact      660
gccgtctatt attgtgtctc gtttggttac tacgtgtctg actatgctat ggctactgg      720
ggtcaaggaa cctcagtcac cgtctcg      747

```

<210> 86

<211> 1072

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 86

```

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1              5              10              15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
20              25              30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
35              40              45

```

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
50              55              60

```

```

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
65              70              75              80

```

```

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
85              90              95

```

```

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
100              105              110

```

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His

580	585	590
Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr 595 600 605		
Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp 610 615 620		
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 625 630 635 640		
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 645 650 655		
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 660 665 670		
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675 680 685		
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 690 695 700		
Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly 705 710 715 720		
Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu 725 730 735		
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala 740 745 750		
Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu 755 760 765		
Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala 770 775 780		
Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu 785 790 795 800		
Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu 805 810 815		

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile Val
 885 890 895

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 900 905 910

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly
 915 920 925

Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
 930 935 940

Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe Ser
 945 950 955 960

Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val Glu
 965 970 975

Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro
 980 985 990

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser
 995 1000 1005

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
 1010 1015 1020

Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
 1025 1030 1035

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp
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I

Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu
 1055 1060 1065

Trp Ile Gly Arg
 1070

<210> 87
 <211> 3429
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 87
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 ccaggggagg tgctggaaaa ggacatcaca cccctgcagg tggttctgcc caacactgcc 360
 ctccatctaa aggcgctgct tgattttgag gataaagatg gagacaaggt ggtggcagga 420
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 gtctcgtga 3429

<210> 88
 <211> 1040
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 88

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 1 5 10 15

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp

115	120	125
Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu 130	135	140
Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val 145	150	155 160
Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu 165	170	175
Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr 180	185	190
Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val 195	200	205
Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys 210	215	220
Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly 225	230	235 240
Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr 245	250	255
Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro 260	265	270
Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met 275	280	285
Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly 290	295	300
Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile 305	310	315 320
Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala 325	330	335
Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln 340	345	350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
 595 600 605

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
 610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 625 630 635 640

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 645 650 655

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 660 665 670

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 675 680 685

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 690 695 700

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
 705 710 715 720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 755 760 765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 770 775 780

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 785 790 795 800

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile

820	825	830
Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu		
835	840	845
Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile Val		
850	855	860
Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala		
865	870	875
Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly		
885	890	895
Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu		
900	905	910
Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe Ser		
915	920	925
Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val Glu		
930	935	940
Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro		
945	950	955
Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser		
965	970	975
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Val		
980	985	990
Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val		
995	1000	1005
Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr		
1010	1015	1020
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile		
1025	1030	1035
Gly Arg		
1040		

<210> 89
 <211> 3333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and *Rattus norvegicus*

<400> 89
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 gagagggtac tgtttgcccc agttcgcatg gtgaccgtcc cccacgcca ctactgcata 180
 gtggccaacc ctgtgtcccg ggacaccag agttctgtgt tatttgacat cacaggacaa 240
 gtccgactcc ggcacgctga ccaggagatc cgactagccc aggaccctt cccctgtat 300
 ccaggggagg tgctggaaaa ggacatcacc cactgcagg tggttctgcc caacacagca 360
 ctgcatctta aggcgttgct ggactttgag gataagaatg gagacaagg catggcagga 420
 gacgagtggc tatttgaggg acctggcacc tacatccac agaaggaagt ggaagtcgtg 480
 gagatcattc aggccacagt catcaaacag aaccaagcac tgcggctaag ggcccgaag 540
 gagtgccttg accgggaggg caaggggagc gtgacagggt aggagtggct ggtccgatcc 600
 gtgggggctt acctcccagc tgtctttgaa gaggtgctgg atctgggtga tgctgtgatc 660
 cttacagaaa agactgccct gcacctccg gctctgcaga acttcaggga ccttcgggga 720
 gtgctccacc gcaccgggga ggaatggtta gtgacagtgc aggacacaga agcccatgtt 780
 ccagatgtct atgaggaggt gcttggggta gtacccatca ccacctggg acctcgacac 840
 tactgtgtca ttcttgacct aatgggacca gacggcaaga accagctggg acaaaagcgt 900
 gttgtcaagg gagagaagtc ctttttcctc cagccaggag agaggctgga gcgaggcatc 960
 caggatgtgt atgtgctgtc agagcagcag gggctgctac tgaaggcact gcagcccctg 1020
 gaggagggag agagcgagga gaaggctctc catcaggccg gagactgctg gctcatccgt 1080
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 cctctggacc aaaatgaggg catctatgtg caggatgtca agacggggaa ggtgcgggct 1200
 gtgattggaa gcacctacat gctgactcag gatgaagtcc tgtgggaaaa ggagctgcct 1260
 tctgggggtg aggagctgct gaacttgggg catgacctc tggcagacag gggtcagaag 1320
 ggcacagcca agccccttca gccctcagct ccaaggaaca agaccgagt ggtcagctac 1380
 cgtgtcccg acaatgcagc ggtgcaggct tatgactaca gagccaagag agcccgtgtg 1440
 gtctttgggc ccgagctagt gacactggat cctgaggagc agttcacagt attgtccctt 1500

tctgccgggc gaccaagcg tcctcatgcc cgccgtgcac tctgcctact gctgggacct	1560
gattttcttta ctgatgtcat caccatcgaa actgcagatc atgccagggtt gcagctgcag	1620
cttgccctaca actggcactt tgaactgaag aaccggaatg accctgcaga ggcagccaag	1680
cttttctccg tgcctgactt cgtgggtgac gcctgcaagg ccattgcatc ccgagtccgg	1740
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atggctgttt ttggctttga gatgtctgaa gacacaggtc ctgatggcac actcctgccc	1860
aaggctcgag accaggcagt ctttcccaa aacgggctgg tagtcagcag tgtggatgtg	1920
cagtcagtgg agcccgtgga ccagaggacc cgggatgccc ttcagcgcag cgttcagctg	1980
gccatcgaaa ttaccaccaa ctcccaggag gcagcagcca agcacgaggc tcagagactg	2040
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aaagcccgca aggaactctt ggagcttgag gctatgagca tggctgtgga gagcacgggt	2160
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cgagtaaaga aagtacgaga gatggaactg atctatgccc gggcccagtt ggagctggag	2340
gtgagcaagg cgcagcagct tgccaatgtg gaggcaaaga agttcaagga gatgacagag	2400
gcactggggc ccggcaccat cagggacctg gctgtggccg ggccagagat gcagggtgaaa	2460
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ctcttcagca cagccttcgg gttgctgggg ctggggtctg atggtcagcc gccagcacag	2580
aaggacattg tgctgaccca atctccagct tctttggctg tgtctcttgg gcagagggcc	2640
accatgtcct gcagagccgg tgaaagtgtt gatatttttg gcgttgggtt tttgcactgg	2700
taccagcaga aaccaggaca gccacccaaa ctctcatct atcgtgcatc caacctagaa	2760
tctgggatcc ctgtcagggt cagtggcact gggcttagga cagacttcac cctcatcatt	2820
gatcctgtgg aggctgatga tgttgccacc tattactgtc agcaaactaa tgaggatccg	2880
tacacgttcg gaggggggac caagctggaa ataaaaggca gtactagcgg cgggtggctcc	2940
ggggggcggt ccggtggggg cggcagcagc gaggttcagc tacaacagtc tggggcagag	3000
cttgtggagc caggggcctc agtcaagttg tcctgcacag cttctggctt caacattaaa	3060
gacacctata tgcactgggt gaagcagagg cctgaacagg gcctggaatg gattggaagg	3120
attgatcctg cgaatggtaa tagtaaatat gtcccgaagt tccagggcaa ggccactata	3180
acagcagaca catcttccaa cacagcctac ctgcagctca ccagcctgac atctgaggac	3240

actgccgtct attattgtgc tccgtttggt tactacgtgt ctgactatgc tatggcctac 3300
 tgggggtcaag gaacctcagt caccgtctcg tga 3333

<210> 90
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 90

Met Gly Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys
 1 5 10 15

Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala
 20 25 30

Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp
 35 40 45

Leu Lys Trp Trp Glu Leu Arg Ala
 50 55

<210> 91
 <211> 171
 <212> DNA
 <213> Homo sapiens

<400> 91
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 gtttgtatgt atatcgaagc tctggacaaa tatgcttgca actgtgttgt tggttacatc 120
 ggtgagcgtt gccagtatcg cgacctgaaa tgggtgggaac tgcgtgcatg a 171

<210> 92
 <211> 949
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized from two Homo sapiens sequences

<400> 92

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 1 5 10 15

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg

500	505	510
Ala Leu Cys Leu Leu Leu Gly	Pro Asp Phe Phe Thr	Asp Val Ile Thr
515	520	525
Ile Glu Thr Ala Asp His	Ala Arg Leu Gln Leu Gln	Leu Ala Tyr Asn
530	535	540
Trp His Phe Glu Val Asn Asp	Arg Lys Asp Pro Gln Glu Thr	Ala Lys
545	550	555
Leu Phe Ser Val Pro Asp Phe	Val Gly Asp Ala Cys Lys	Ala Ile Ala
565	570	575
Ser Arg Val Arg Gly Ala Val	Ala Ser Val Thr Phe Asp	Asp Phe His
580	585	590
Lys Asn Ser Ala Arg Ile Ile	Arg Thr Ala Val Phe Gly	Phe Glu Thr
595	600	605
Ser Glu Ala Lys Gly Pro Asp	Gly Met Ala Leu Pro Arg	Pro Arg Asp
610	615	620
Gln Ala Val Phe Pro Gln Asn	Gly Leu Val Val Ser Ser	Val Asp Val
625	630	635
Gln Ser Val Glu Pro Val Asp	Gln Arg Thr Arg Asp	Ala Leu Gln Arg
645	650	655
Ser Val Gln Leu Ala Ile Glu	Ile Thr Thr Asn Ser Gln	Glu Ala Ala
660	665	670
Ala Lys His Glu Ala Gln Arg	Leu Glu Gln Glu Ala Arg	Gly Arg Leu
675	680	685
Glu Arg Gln Lys Ile Leu Asp	Gln Ser Glu Ala Glu Lys	Ala Arg Lys
690	695	700
Glu Leu Leu Glu Leu Glu Ala	Leu Ser Met Ala Val Glu	Ser Thr Gly
705	710	715
Thr Ala Lys Ala Glu Ala Glu	Ser Arg Ala Glu Ala Ala	Arg Ile Glu
725	730	735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
 755 760 765

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 770 775 780

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
 785 790 795 800

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly Asn
 885 890 895

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 900 905 910

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
 915 920 925

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
 930 935 940

Trp Glu Leu Arg Ala
 945

<210> 93
 <211> 2850

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized from two Homo sapiens sequences

<400> 93

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gagaggggtac tgtttgcccc catgcgcacg gtgaccgtcc cccacgtca ctactgcaca	180
gtggccaacc ctgtgtctcg ggatgccag ggcttggtgc tgttgatgt cacagggcaa	240
gttcggcttc gccacgtga cctcgagac cggctggccc aggaccctt cccctgtac	300
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ctccatctaa aggcgctgct tgattttgag gataaagatg gagacaaggt ggtggcagga	420
gatgagtggc ttttcgaggg acctggcacg tacatcccc ggaaggaagt ggaggtcgtg	480
gagatcattc aggccaccat catcaggcag aaccaggctc tgcggctcag ggcccgcaag	540
gagtgctggg accgggacgg caaggagagg gtgacagggg aagaatggct ggtcaccaca	600
gtaggggctg acctccagc ggtgtttgag gaggttctgg atttggtgga cgccgtcatc	660
cttacggaaa agacagccct gcacctcgg gctcggcgga acttccggga cttcagggga	720
gtgtcccgcc gactgggga ggagtggctg gtaacagtgc aggacacaga ggccacgtg	780
ccagatgtcc acgaggaggt gctgggggtt gtgcccata ccaccctggg ccccccacaac	840
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gtggtcaagg gagagaagtc ttttttcctc cagccaggag agcagctgga acaaggcatc	960
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tcagctgggc ggccaagcg tccccatgcc cgcgctgcgc tctgcctgct gctggggcct	1560

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gacctgaaat ggtgggaact gcgtgcatga 2850

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<210> 94

<211> 917

<212> PRT

<213> Artificial Sequence

<220>

<223> Rattus norvegicus and Homo sapiens

<400> 94

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Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10           15

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His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr

485	490	495
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg 500	505	510
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr 515	520	525
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn 530	535	540
Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys 545	550	555
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala 565	570	575
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His 580	585	590
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met 595	600	605
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp 610	615	620
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 625	630	635
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 645	650	655
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 660	665	670
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675	680	685
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 690	695	700
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly 705	710	715
		720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 755 760 765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 770 775 780

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 785 790 795 800

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Met Gly Asn
 850 855 860

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 865 870 875 880

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
 885 890 895

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
 900 905 910

Trp Glu Leu Arg Ala
 915

<210> 95

<211> 2754

<212> DNA

<213> Artificial Sequence

<220>

<223> *Rattus norvegicus* and *Homo sapiens*

<400> 95

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<210> 96

<211> 1005

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Homo sapiens* and *Drosophila melanogaster*

<400> 96

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20          25          30

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35          40          45

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Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
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Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
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Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
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Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
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Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
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Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr

275	280	285
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Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly		
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Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr		
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Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro		
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Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val		
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Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly		
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Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile		
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Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala		
420	425	430
Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln		
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Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser		
450	455	460
Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu		
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Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala		
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Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu		
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Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
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Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
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Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
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Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
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Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
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Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
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Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
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Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
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Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
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Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
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Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Arg Gln Ile

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985

990

Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
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<210> 97
 <211> 3018
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Saccaromyces cerevisiae* and *Homo sapiens* and *Drosophila melanogaster*

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3018

<210> 98
 <211> 973
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<220>
 <223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Drosophila melanogaster*

<400> 98

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
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Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
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Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
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Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
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Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
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Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
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Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 530 535 540

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
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Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys

645	650	655
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala 660 665 670		
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His 675 680 685		
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met 690 695 700		
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp 705 710 715 720		
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 725 730 735		
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 740 745 750		
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 755 760 765		
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 770 775 780		
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 785 790 795 800		
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly 805 810 815		
Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu 820 825 830		
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala 835 840 845		
Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met 850 855 860		
Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala 865 870 875 880		

304/429

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gccttcgggt tgctggggct ggggtctgat ggtcagccgc cagcacagaa gcgacagatc 2880
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<400> 100

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Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20           25           30

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35           40           45

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Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
50           55           60

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Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65           70           75           80

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Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85           90           95

```

```

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
100          105          110

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
115          120          125

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Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 530 535 540

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg

595

600

605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
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Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
 850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
 885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
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Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile Val
 980 985 990

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 995 1000 1005

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val
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Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys
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Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile
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Asp Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln
 1070 1075 1080

Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 1085 1090 1095

Ile Lys Gly Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
 1100 1105 1110

Gly Gly Gly Ser Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu
 1115 1120 1125

Leu Val Glu Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser
 1130 1135 1140

Gly Phe Asn Ile Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg
 1145 1150 1155

Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn
 1160 1165 1170

Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile
 1175 1180 1185

Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser
 1190 1195 1200

Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly
 1205 1210 1215

Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
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Ser Val Thr Val Ser
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<211> 1206

<212> PRT

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<223> synthesized and *Saccharomyces cerevisiae* and *Rattus norvegicus*

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 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 530 535 540

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn

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Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys			
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Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala			
660		665	670
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His			
675	680		685
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met			
690	695	700	
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp			
705	710	715	720
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val			
725	730		735
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg			
740	745		750
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala			
755	760		765
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu			
770	775	780	
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys			
785	790	795	800
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly			
805	810		815
Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu			
820	825		830
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala			
835	840		845
Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met			
850	855	860	

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile Val
 945 950 955 960

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 965 970 975

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly
 980 985 990

Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
 995 1000 1005

Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe
 1010 1015 1020

Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro
 1025 1030 1035

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
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Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 1055 1060 1065

Gly Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 1070 1075 1080

Gly Ser Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val
 1085 1090 1095

Glu Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe
 1100 1105 1110

Asn Ile Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu
 1115 1120 1125

Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn
 1130 1135 1140

Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala
 1145 1150 1155

Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr
 1160 1165 1170

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr
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Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr Ser Val
 1190 1195 1200

Thr Val Ser
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<210> 104

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and two *Homo sapiens* sequences

<400> 104

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 225 230 235 240

465 470 475 480
 Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495
 Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
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 Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 515 520 525
 Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 530 535 540
 Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560
 Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 565 570 575
 Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 580 585 590
 Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605
 Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
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 Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
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 Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
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 675 680 685
 Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
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Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly Asn
 980 985 990

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 995 1000 1005

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 1010 1015 1020

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu
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Lys Trp Trp Glu Leu Arg Ala
 1040 1045

<210> 105
 <211> 3138
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Saccaromyces cerevisiae* and two *Homo sapiens* sequences

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<210> 106

<211> 1013

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Homo sapiens*

<400> 106

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
305 310 315 320

545	550	555	560
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Val Phe Gly Pro	Glu Leu Val Thr	Leu Asp Pro Glu	Glu Gln Phe Thr
	580	585	590
Val Leu Ser Leu	Ser Ala Gly Arg	Pro Lys Arg Pro	His Ala Arg Arg
	595	600	605
Ala Leu Cys Leu	Leu Leu Gly Pro	Asp Phe Phe Thr	Asp Val Ile Thr
	610	615	620
Ile Glu Thr Ala	Asp His Ala Arg	Leu Gln Leu Gln	Leu Ala Tyr Asn
	625	630	635
Trp His Phe Glu	Leu Lys Asn Arg	Asn Asp Pro Ala	Glu Ala Ala Lys
	645	650	655
Leu Phe Ser Val	Pro Asp Phe Val	Gly Asp Ala Cys	Lys Ala Ile Ala
	660	665	670
Ser Arg Val Arg	Gly Ala Val Ala	Ser Val Thr Phe	Asp Asp Phe His
	675	680	685
Lys Asn Ser Ala	Arg Ile Ile Arg	Met Ala Val Phe	Gly Phe Glu Met
	690	695	700
Ser Glu Asp Thr	Gly Pro Asp Gly	Thr Leu Leu Pro	Lys Ala Arg Asp
	705	710	715
Gln Ala Val Phe	Pro Gln Asn Gly	Leu Val Val Ser	Ser Val Asp Val
	725	730	735
Gln Ser Val Glu	Pro Val Asp Gln	Arg Thr Arg Asp	Ala Leu Gln Arg
	740	745	750
Ser Val Gln Leu	Ala Ile Glu Ile	Thr Thr Asn Ser	Gln Glu Ala Ala
	755	760	765
Ala Lys His Glu	Ala Gln Arg Leu	Glu Gln Glu Ala	Arg Gly Arg Leu
	770	775	780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
 805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Met Gly Asn
 945 950 955 960

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 965 970 975

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
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Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
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Trp Glu Leu Arg Ala
 1010

<210> 107
 <211> 3042
 <212> DNA
 <213> Artificial Sequence

<220>

<223> *Saccharomyces cerevisiae* and *Rattus norvegicus* and *Homo sapiens*

<400> 107

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tatatcgaag ctctggacaa atatgcttgc aactgtgttg ttggttacat cgggtgagcgt 3000
tgccagtatc gcgacctgaa atgggtgggaa ctgcgtgcat ga 3042

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<210> 108
<211> 1000
<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Homo sapiens* and Human immunodeficiency virus type 1

<400> 108

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
 1 5 10 15

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln

435	440	445	
Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser			
450	455	460	
Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu			
465	470	475	480
Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala			
485	490	495	
Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu			
500	505	510	
Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp			
515	520	525	
Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro			
530	535	540	
Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His			
545	550	555	560
Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val			
565	570	575	
Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr			
580	585	590	
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg			
595	600	605	
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr			
610	615	620	
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn			
625	630	635	640
Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys			
645	650	655	
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala			
660	665	670	

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
 805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
 850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
 885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Tyr Gly Arg
 980 985 990

Lys Lys Arg Arg Gln Arg Arg Arg
 995 1000

<210> 109
 <211> 3003
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Saccaromyces cerevisiae* and *Homo sapiens* and Human
 immunodeficiency virus type 1

<400> 109
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 tctcccaaaa ccaaaggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180
 ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240
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 gagttcatca tccgcatccc ccataccac tatatccatg tgctggacca gaacagcaac 360
 gtgtcccgtg tggaggtcgg gccaaagacc tacatccggc aggacaatga gaggggtactg 420
 tttgccccca tgcgcatggt gaccgtcccc ccacgtcact actgcacagt ggccaaccct 480
 gtgtctcggg atgcccaggg cttggtgctg tttgatgtca cagggaagt tcggcttcgc 540
 cacgtgacc tcgagatccg gctggcccag gacccttcc ccctgtaccc aggggaggtg 600
 ctggaaaagg acatcacacc cctgcaggtg gttctgccc aactgccct ccatctaaag 660
 gcgctgcttg attttgagga taaagatgga gacaaggtgg tggcaggaga tgagtggctt 720

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gccaccatca tcaggcagaa ccaggctctg	cggctcaggg cccgcaagga gtgctgggac	840
cgggacggca aggagagggt gacaggggaa	gaatggctgg tcaccacagt aggggcgtac	900
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gaacttttgg agctggaggc tctgagcatg	gccgtggaga gcaccgggac tgccaaggcg	2460


```

gaggccgagt cccgtgcgga ggcagcccgg attgagggag aaggggccgt gctgcaggcc 2520
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tga 3003

```

```

<210> 110
<211> 968
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Saccharomyces cerevisiae and Rattus norvegicus and Human
immunodeficiency virus type 1

```

```

<400> 110

```

```

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
1           5           10           15

```

```

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20           25           30

```

```

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35           40           45

```

```

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
50           55           60

```

```

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65           70           75           80

```

```

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85           90           95

```

```

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
100          105          110

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr

340	345	350
Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro		
355	360	365
Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met		
370	375	380
Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly		
385	390	395
400		
Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile		
405	410	415
Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala		
420	425	430
Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln		
435	440	445
Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser		
450	455	460
Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln		
465	470	475
480		
Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala		
485	490	495
Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu		
500	505	510
Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp		
515	520	525
Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro		
530	535	540
Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His		
545	550	555
560		
Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val		
565	570	575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
 690 695 700

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
 805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Tyr Gly Arg
 945 950 955 960

Lys Lys Arg Arg Gln Arg Arg Arg
 965

<210> 111

<211> 2907

<212> DNA

<213> Artificial Sequence

<220>

<223> Saccaromyces cerevisiae and Rattus norvegicus and Human
 immunodeficiency virus type 1

<400> 111

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tctcccaaaa ccaaaagggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180

ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240

ttgaaaatgg attctttaca ggatataaaa gcattgttaa caggattaat ggcaactgaa	300
gaggccatca tccgcattccc cccataccac tacatccatg tgctggacca gaacagtaat	360
gtgtcccgtg tggaggttgg accaaagacc tacatccggc aggacaatga gaggggtactg	420
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cacgctgacc aggagatccg actagcccag gacccttcc cctgtatcc aggggaggtg	600
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gccacagtca tcaaacagaa ccaagcactg cggctaaggg cccgaaagga gtgctttgac	840
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<210> 112
 <211> 1040
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens and Drosophila melanogaster

<400> 112

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Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
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```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20           25          30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35           40          45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50           55          60

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr
130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
165 170 175

Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val
180 185 190

Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val
195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala
210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
245 250 255

Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp
260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val
275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala
290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu
305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu
325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp
355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val
370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly
385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu
405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu
435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
450 455 460

Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val
465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr
485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val

530	535	540
Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys		
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Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser		
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Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg		
	580	585 590
Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg		
	595	600 605
Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu		
	610	615 620
Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His		
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Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp		
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Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu		
	660	665 670
Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu		
	675	680 685
Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys		
	690	695 700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp		
705	710	715 720
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly		
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Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg		
	740	745 750
Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser		
	755	760 765

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln
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Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg
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Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu
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Ser Thr Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala
 850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln
 865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val
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Arg Glu Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln
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Met Thr Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
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Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala
 965 970 975

Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg
 980 985 990

Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala
 995 1000 1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu
 1010 1015 1020

Arg Arg Gln Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp
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Lys Lys
 1040

<210> 113
 <211> 3123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens and Drosophila melanogaster

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tga 3123

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<210> 114

<211> 1008

<212> PRT

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and Drosophila melanogaster

<400> 114

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Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1           5           10           15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
          20           25           30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
      35           40           45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
      50           55           60

```

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
      65           70           75           80

```

```

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
          85           90           95

```

```

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
          100          105          110

```

```

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
          115          120          125

```

```

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr
          130          135          140

```

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
 165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val
 180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile
 195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala
 210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
 225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
 245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp
 260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val
 530 535 540

Leu Trp Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu
 545 550 555 560

Gly His Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro
 565 570 575

Leu Gln Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu

610	615	620
Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His		
625	630	635 640
Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp		
	645	650 655
Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu		
	660	665 670
Ala Tyr Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu		
	675	680 685
Ala Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys		
	690	695 700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp		
	705	710 715 720
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly		
	725	730 735
Phe Glu Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys		
	740	745 750
Ala Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser		
	755	760 765
Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala		
	770	775 780
Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln		
	785	790 795 800
Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg		
	805	810 815
Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys		
	820	825 830
Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu		
	835	840 845

Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala
850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln
865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val
885 890 895

Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
900 905 910

Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu
915 920 925

Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala
930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala
965 970 975

Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
980 985 990

Arg Gln Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
995 1000 1005

<210> 115

<211> 3027

<212> DNA

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and Drosophila melanogaster

<400> 115

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caggcttaca aagtaacctg tagcgttcgt cagagctctg cgcagaatcg caaatacacc	180
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gccgcatggc gttcgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc	300

gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360
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<210> 116

<211> 1273

<212> PRT

<213> Artificial Sequence

<220>

<223> Levivirus and Homo sapiens and synthesized

<400> 116

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Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
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```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20           25           30

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```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35           40           45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu

```

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 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80
 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95
 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110
 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125
 Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr
 130 135 140
 His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
 145 150 155 160
 Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
 165 170 175
 Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val
 180 185 190
 Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val
 195 200 205
 Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala
 210 215 220
 Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
 225 230 235 240
 Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
 245 250 255
 Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp
 260 265 270
 Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp
 355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu
 435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
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Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
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Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val
 530 535 540

Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys
 545 550 555 560

Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser
 565 570 575

Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu
 610 615 620

Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His
 625 630 635 640

Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp
 645 650 655

Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu
 660 665 670

Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu
 675 680 685

Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys
 690 695 700

Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp
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Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly
 725 730 735

Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg
 740 745 750

Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser

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900					905					910									
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915					920					925									
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Gly	Pro	Glu	Met	Gln	Val	Lys	Leu	Leu	Gln	Ser	Leu	Gly	Leu	Lys	Ser				
945					950					955					960				
Thr	Leu	Ile	Thr	Asp	Gly	Ser	Thr	Pro	Ile	Asn	Leu	Phe	Asn	Thr	Ala				
965					970					975									
Phe	Gly	Leu	Leu	Gly	Met	Gly	Pro	Glu	Gly	Gln	Pro	Leu	Gly	Arg	Arg				
980					985					990									

Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala
 995 1000 1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu
 1010 1015 1020

Arg Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser
 1025 1030 1035

Leu Gly Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val
 1040 1045 1050

Asp Ile Phe Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro
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Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu
 1070 1075 1080

Ser Gly Ile Pro Val Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp
 1085 1090 1095

Phe Thr Leu Ile Ile Asp Pro Val Glu Ala Asp Asp Val Ala Thr
 1100 1105 1110

Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gly
 1115 1120 1125

Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Gly Gly Ser
 1130 1135 1140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Val Gln Leu Gln
 1145 1150 1155

Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys Leu
 1160 1165 1170

Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
 1175 1180 1185

Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg
 1190 1195 1200

Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln
 1205 1210 1215

Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
 1220 1225 1230

Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr
 1235 1240 1245

Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr
 1250 1255 1260

Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 1265 1270

<210> 117

<211> 3822

<212> DNA

<213> Artificial Sequence

<220>

<223> Levivirus and Homo sapiens and synthesized

<400> 117

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<210> 118

<211> 1241

<212> PRT

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and synthesized

<400> 118

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser

35	40	45
Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu		
50	55	60
Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val		
65	70	75
Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe		
85	90	95
Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu		
100	105	110
Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly		
115	120	125
Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr		
130	135	140
His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu		
145	150	155
Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe		
165	170	175
Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val		
180	185	190
Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile		
195	200	205
Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala		
210	215	220
Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile		
225	230	235
Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala		
245	250	255
Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp		
260	265	270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

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<210> 126

<211> 1003

<212> PRT

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and Human immunodeficiency virus type 1

<400> 126

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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
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Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr
 130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
 165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val
 180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile
 195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala
 210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
 225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
 245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp
 260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro

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Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys 515	520	525
Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val 530	535	540
Leu Trp Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu 545	550	555 560
Gly His Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro 565	570	575
Leu Gln Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg 580	585	590
Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg 595	600	605
Ala Arg Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu 610	615	620
Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His 625	630	635 640
Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp 645	650	655
Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu 660	665	670
Ala Tyr Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu 675	680	685
Ala Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys 690	695	700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp 705	710	715 720
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly 725	730	735

Phe Glu Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys
 740 745 750

Ala Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser
 755 760 765

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln
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Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg
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Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu
 835 840 845

Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala
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Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln
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Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val
 885 890 895

Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu
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Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
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Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala
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Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
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Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
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<210> 127

<211> 3012

<212> DNA

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and Human immunodeficiency virus
 type 1

<400> 127

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gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc      360
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ctgg	ctgtgg	ccggg	ccaga	gatgc	aggtg	aaact	tctcc	agtc	ccctggg	cctga	aatcc	2880
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aggcgacggt ga 3012

<210> 128
<211> 926
<212> PRT
<213> Artificial Sequence

<220>
<223> synthesized and Homo sapiens and Drosophila melanogaster
<400> 128

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20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu
 610 615 620

Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp

645					650					655									
Val	Gln	Ser	Val	Glu	Pro	Val	Asp	Gln	Arg	Thr	Arg	Asp	Ala	Leu	Gln				
660					665					670									
Arg	Ser	Val	Gln	Leu	Ala	Ile	Glu	Ile	Thr	Thr	Asn	Ser	Gln	Glu	Ala				
675					680					685									
Ala	Ala	Lys	His	Glu	Ala	Gln	Arg	Leu	Glu	Gln	Glu	Ala	Arg	Gly	Arg				
690					695					700									
Leu	Glu	Arg	Gln	Lys	Ile	Leu	Asp	Gln	Ser	Glu	Ala	Glu	Lys	Ala	Arg				
705					710					715					720				
Lys	Glu	Leu	Leu	Glu	Leu	Glu	Ala	Leu	Ser	Met	Ala	Val	Glu	Ser	Thr				
725					730					735									
Gly	Thr	Ala	Lys	Ala	Glu	Ala	Glu	Ser	Arg	Ala	Glu	Ala	Ala	Arg	Ile				
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Glu	Gly	Glu	Gly	Ser	Val	Leu	Gln	Ala	Lys	Leu	Lys	Ala	Gln	Ala	Leu				
755					760					765									
Ala	Ile	Glu	Thr	Glu	Ala	Glu	Leu	Gln	Arg	Val	Gln	Lys	Val	Arg	Glu				
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Leu	Glu	Leu	Val	Tyr	Ala	Arg	Ala	Gln	Leu	Glu	Leu	Glu	Val	Ser	Lys				
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Ala	Gln	Gln	Leu	Ala	Glu	Val	Glu	Val	Lys	Lys	Phe	Lys	Gln	Met	Thr				
805					810					815									
Glu	Ala	Ile	Gly	Pro	Ser	Thr	Ile	Arg	Asp	Leu	Ala	Val	Ala	Gly	Pro				
820					825					830									
Glu	Met	Gln	Val	Lys	Leu	Leu	Gln	Ser	Leu	Gly	Leu	Lys	Ser	Thr	Leu				
835					840					845									
Ile	Thr	Asp	Gly	Ser	Thr	Pro	Ile	Asn	Leu	Phe	Asn	Thr	Ala	Phe	Gly				
850					855					860									
Leu	Leu	Gly	Met	Gly	Pro	Glu	Gly	Gln	Pro	Leu	Gly	Arg	Arg	Val	Ala				
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Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
915 920 925

<220>
<223> synthesized and Homo sapiens and Drosophila melanogaster

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<210> 130

<211> 894

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus and Drosophila melanogaster

<400> 130

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Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val

195	200	205
Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala		
210	215	220
Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu		
225	230	235 240
Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg		
245	250	255
Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp		
260	265	270
Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val		
275	280	285
Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro		
290	295	300
Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys		
305	310	315 320
Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly		
325	330	335
Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys		
340	345	350
Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His		
355	360	365
Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro		
370	375	380
Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp		
385	390	395 400
Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg		
405	410	415
Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp		
420	425	430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
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Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr
725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu
770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr
805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly
850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Arg Gln
865 870 875 880

Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
885 890

<210> 131

<211> 2685
 <212> DNA
 <213> Artificial Sequence

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<223> synthesized and *Rattus norvegicus* and *Drosophila melanogaster*

<400> 131

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gaggagctgc tgaacttggg gcatgaccct ctggcagaca ggggtcagaa gggcacagcc	1380
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cacaatgcag cgggtgcaggt ctatgactac agagccaaga gagcccgtgt ggtctttggg	1500

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<210> 132

<211> 1159

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 132

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Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1          5          10          15

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```

Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20          25          30

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Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe

500

505

510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu
 610 615 620

Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr
 725 730 735

Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu
 770 775 780

Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr
 805 810 815

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala
 865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
 885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile
 900 905 910

Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
 915 920 925

Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val
 930 935 940

Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
 945 950 955 960

Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe
 965 970 975

Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val
 980 985 990

Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp
 995 1000 1005

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser
 1010 1015 1020

Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1025 1030 1035

Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro
 1040 1045 1050

Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
 1055 1060 1065

Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly
 1070 1075 1080

Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys
 1085 1090 1095

Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr
 1100 1105 1110

Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr Ser Glu
 1115 1120 1125

Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val Ser
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Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
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Ser

<210> 133
 <211> 3480
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 133

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ccgaagttcc agggcaaggc cactataaca gcagacacat cttccaacac agcctacctg	3360

cagctcacca gcctgacatc tgaggacact gccgtctatt attgtgctcc gtttggttac 3420

tacgtgtctg actatgctat ggcctactgg ggtcaaggaa cctcagtcac cgtctcgtga 3480

<210> 134

<211> 1127

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus

<400> 134

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
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Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr
20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val
165 170 175

Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg
 245 250 255

Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp

645	650	655
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln		
660	665	670
Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala		
675	680	685
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg		
690	695	700
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg		
705	710	715
Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr		
725	730	735
Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile		
740	745	750
Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu		
755	760	765
Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu		
770	775	780
Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys		
785	790	795
Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr		
805	810	815
Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro		
820	825	830
Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu		
835	840	845
Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly		
850	855	860
Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile		
865	870	875
		880

Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
 885 890 895

Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val
 900 905 910

Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
 915 920 925

Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe
 930 935 940

Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val
 945 950 955 960

Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp
 965 970 975

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr
 980 985 990

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
 995 1000 1005

Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
 1010 1015 1020

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp
 1025 1030 1035

Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu
 1040 1045 1050

Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val
 1055 1060 1065

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser
 1070 1075 1080

Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr
 1085 1090 1095

Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr
 1100 1105 1110

Ala Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 1115 1120 1125

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 <211> 3384
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 135
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 cctgtgtccc gggacaccca gagttctgtg ttatttgaca tcacaggaca agtccgactc 300
 cggcacgctg accaggagat ccgactagcc caggaccctt tccccctgta tccaggggag 360
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 aaggcgttgc tggactttga ggataagaat ggagacaagg tcatggcagg agacgagtgg 480
 ctatttgagg gacctggcac ctacatccca cagaaggaag tggaagtcgt ggagatcatt 540
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 gaccgggagg gcaaggggag cgtgacaggt gaggagtggc tgggtccgatc cgtgggggct 660
 tacctcccag ctgtctttga agaggtgctg gatctgggtg atgctgtgat ccttacagaa 720
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 cgcaccgggg aggaatggtt agtgacagtg caggacacag aagcccatgt tccagatgtc 840
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 caaaatgagg gcatctatgt gcaggatgtc aagacgggga aggtgcgggc tgtgattgga 1260
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gccaaactca aggcacaggc gctagccatt gagacggagg ctgagttgga gcgagtaaag 2340
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ggagggggga ccaagctgga aataaaaggc agtactagcg gcggtggctc cggggcggt 3000
tccggtgggg gcggcagcag cgaggttcag ctacaacagt ctggggcaga gcttgtggag 3060


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ccaggggcct cagtcaagtt gtctgcaca gcttctggct tcaacattaa agacacctat 3120
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<210> 136

<211> 966

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and two Homo sapiens sequences

<400> 136

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Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1          5          10          15

```

```

Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20          25          30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
          35          40          45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
          50          55          60

```

```

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
65          70          75          80

```

```

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
          85          90          95

```

```

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
          100          105          110

```

```

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
          115          120          125

```

```

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
          130          135          140

```

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu

610	615	620
Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg 625 630 635 640		
Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp 645 650 655		
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln 660 665 670		
Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala 675 680 685		
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg 690 695 700		
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg 705 710 715 720		
Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr 725 730 735		
Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile 740 745 750		
Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu 755 760 765		
Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu 770 775 780		
Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys 785 790 795 800		
Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr 805 810 815		
Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro 820 825 830		
Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu 835 840 845		

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly
850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala
865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly
900 905 910

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
915 920 925

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
930 935 940

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
945 950 955 960

Trp Trp Glu Leu Arg Ala
965

<210> 137
<211> 2901
<212> DNA
<213> Artificial Sequence

<220>
<223> synthesized and two Homo sapiens sequences

<400> 137
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ctgtttgccc ccatgcgcat ggtgaccgtc cccccacgtc actactgcac agtggccaac 240
cctgtgtctc gggatgccca gggcttggtg ctgtttgatg tcacagggca agttcggctt 300
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aaggcgctgc ttgattttga ggataaagat ggagacaagg tggaggcagg agatgagtgg 480
cttttcgagg gacctggcac gtacatcccc cggaaggaag tggaggtcgt ggagatcatt 540

caggccacca tcatcaggca gaaccaggct ctgcggtca gggccgcaa ggagtgtctgg 600
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gccaaagctaa aagcacaggc cttggccatt gaaacggagg ctgagctcca gaggggtccag 2340
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<210> 138

<211> 934

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus and Homo sapiens

<400> 138

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Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1          5          10          15

```

```

Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20          25          30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
          35          40          45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
          50          55          60

```

```

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
65          70          75          80

```

```

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
          85          90          95

```

```

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp

```

100	105	110
Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro		
115	120	125
Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu		
130	135	140
Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp		
145	150	155
Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val		
165	170	175
Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg		
180	185	190
Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val		
195	200	205
Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala		
210	215	220
Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu		
225	230	235
Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg		
245	250	255
Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp		
260	265	270
Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val		
275	280	285
Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro		
290	295	300
Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys		
305	310	315
Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly		
325	330	335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr
 725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu
 770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr

805					810					815					
Glu	Ala	Leu	Gly	Pro	Gly	Thr	Ile	Arg	Asp	Leu	Ala	Val	Ala	Gly	Pro
			820					825					830		
Glu	Met	Gln	Val	Lys	Leu	Leu	Gln	Ser	Leu	Gly	Leu	Lys	Ser	Thr	Leu
			835				840					845			
Ile	Thr	Asp	Gly	Ser	Ser	Pro	Ile	Asn	Leu	Phe	Ser	Thr	Ala	Phe	Gly
			850				855					860			
Leu	Leu	Gly	Leu	Gly	Ser	Asp	Gly	Gln	Pro	Pro	Ala	Gln	Lys	Met	Gly
			865				870					875			880
Asn	Ser	Asp	Ser	Glu	Cys	Pro	Leu	Ser	His	Asp	Gly	Tyr	Cys	Leu	His
				885					890					895	
Asp	Gly	Val	Cys	Met	Tyr	Ile	Glu	Ala	Leu	Asp	Lys	Tyr	Ala	Cys	Asn
				900				905						910	
Cys	Val	Val	Gly	Tyr	Ile	Gly	Glu	Arg	Cys	Gln	Tyr	Arg	Asp	Leu	Lys
				915				920						925	
Trp	Trp	Glu	Leu	Arg	Ala										
				930											

<210> 139
 <211> 2805
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus and Homo sapiens

<400> 139
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 aatgtgtccc gtgtggaggt tggaccaaag acctacatcc ggcaggacaa tgagagggta 180
 ctgtttgccc cagttcgcgc ggtgaccgtc cccccacgcc actactgcat agtggccaac 240
 cctgtgtccc gggacaccca gagttctgtg ttatttgaca tcacaggaca agtccgactc 300
 cggcacgctg accaggagat ccgactagcc caggaccctt tccccctgta tccagggggag 360
 gtgctggaaa aggacatcac ccactgcag gtggttctgc ccaacacagc actgcatctt 420

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cgacccaagc gtccctatgc ccgccgtgca ctctgcctac tgctgggacc tgatttcttt	1620
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gcctctgtca cttttgatga cttccataaa aactcagccc ggatcattcg aatggctgtt	1860
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gagcccgtgg accagaggac ccgggatgcc cttcagcgca gcgttcagct ggccatcgaa	2040
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<210> 140

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens and Human immunodeficiency virus
type 1

<400> 140

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Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1           5           10           15

```

```

Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20           25           30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
          35           40           45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
          50           55           60

```

```

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
65           70           75           80

```

```

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
          85           90           95

```

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala

565					570					575					
Lys	Leu	Phe	Ser	Val	Pro	Asp	Phe	Val	Gly	Asp	Ala	Cys	Lys	Ala	Ile
			580					585					590		
Ala	Ser	Arg	Val	Arg	Gly	Ala	Val	Ala	Ser	Val	Thr	Phe	Asp	Asp	Phe
			595				600					605			
His	Lys	Asn	Ser	Ala	Arg	Ile	Ile	Arg	Thr	Ala	Val	Phe	Gly	Phe	Glu
	610					615					620				
Thr	Ser	Glu	Ala	Lys	Gly	Pro	Asp	Gly	Met	Ala	Leu	Pro	Arg	Pro	Arg
625					630					635					640
Asp	Gln	Ala	Val	Phe	Pro	Gln	Asn	Gly	Leu	Val	Val	Ser	Ser	Val	Asp
				645					650					655	
Val	Gln	Ser	Val	Glu	Pro	Val	Asp	Gln	Arg	Thr	Arg	Asp	Ala	Leu	Gln
			660					665					670		
Arg	Ser	Val	Gln	Leu	Ala	Ile	Glu	Ile	Thr	Thr	Asn	Ser	Gln	Glu	Ala
		675					680					685			
Ala	Ala	Lys	His	Glu	Ala	Gln	Arg	Leu	Glu	Gln	Glu	Ala	Arg	Gly	Arg
	690					695					700				
Leu	Glu	Arg	Gln	Lys	Ile	Leu	Asp	Gln	Ser	Glu	Ala	Glu	Lys	Ala	Arg
705					710					715					720
Lys	Glu	Leu	Leu	Glu	Leu	Glu	Ala	Leu	Ser	Met	Ala	Val	Glu	Ser	Thr
				725					730					735	
Gly	Thr	Ala	Lys	Ala	Glu	Ala	Glu	Ser	Arg	Ala	Glu	Ala	Ala	Arg	Ile
			740					745					750		
Glu	Gly	Glu	Gly	Ser	Val	Leu	Gln	Ala	Lys	Leu	Lys	Ala	Gln	Ala	Leu
		755					760					765			
Ala	Ile	Glu	Thr	Glu	Ala	Glu	Leu	Gln	Arg	Val	Gln	Lys	Val	Arg	Glu
	770					775					780				
Leu	Glu	Leu	Val	Tyr	Ala	Arg	Ala	Gln	Leu	Glu	Leu	Glu	Val	Ser	Lys
785					790					795					800

Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr
 805 810 815

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala
 865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
 885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Tyr Gly
 900 905 910

Arg Lys Lys Arg Arg Gln Arg Arg Arg
 915 920

<210> 141
 <211> 2766
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens and Human immunodeficiency virus
 type 1

<400> 141
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gaccgggacg gcaaggagag ggtgacaggg gaagaatggc tggtcaccac agtaggggag	660
tacctcccag cgggtgtttga ggaggttctg gatttggtgg acgccgtcat ccttacggaa	720
aagacagccc tgcacctccg ggctcggcgg aacttcgggg acttcagggg agtgtcccgc	780
cgcactgggg aggagtggct ggtaacagtg caggacacag agggccacgt gccagatgtc	840
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```

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cggtga 2766

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<210> 142

<211> 889

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus and Human immunodeficiency virus type 1

<400> 142

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Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1          5          10          15

```

```

Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20          25          30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
          35          40          45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
          50          55          60

```

```

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
65          70          75          80

```

```

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
          85          90          95

```

```

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
          100          105          110

```

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg
 245 250 255

Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys

340	345	350
Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His		
355	360	365
Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro		
370	375	380
Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp		
385	390	395
Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg		
405	410	415
Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp		
420	425	430
Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His		
435	440	445
Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln		
450	455	460
Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro		
465	470	475
His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg		
485	490	495
Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe		
500	505	510
Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg		
515	520	525
Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile		
530	535	540
Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr		
545	550	555
Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala		
565	570	575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr
 725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu
 770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr
 805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Tyr Gly
 865 870 875 880

Arg Lys Lys Arg Arg Gln Arg Arg Arg
 885

<210> 143

<211> 2670

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus and Human immunodeficiency virus type 1

<400> 143

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